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F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD)//0.60:25:48//MEGABOMBUS PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE)//P04567

5 F-PLACE1010329//TOXIN S5C10//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA)//P01419

10 F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.0049:49:55//HOMO SAPIENS (HUMAN)//P39189

15 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE) (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC)//0.0034:89:30//TRYPANOSOMA CRUZI//015886

20 F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B17) (CI-B17)//1.0:40:35//SUS SCROFA (PIG)//Q29259

F-PLACE1010383

25 F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140)//0.10:174:22//RATTUS NORVEGICUS (RAT)//P41777

30 F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III//1.5e-21:170:35//CAENORHABDITIS ELEGANS//P46555

F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//1.0:31:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40490

35 F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I//0.77:97:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09874

40 F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.74:45:37//HOMO SAPIENS (HUMAN)//P22531

45 F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)]//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN) //P32296

50 F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION//0.17:68:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53227

55 F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33//0.50:48:29//PORPHYRA PURPUREA//P51255

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- F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571.//0.29:37:43//HAEMOPHILUS INFLUENZAE.//P44260
- 5 F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//3.3e-38:178:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747
- 10 F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14).//4.6e-17:192:31//PICHIA ANGUSTA (YEAST) (HANSENULA POLYMORPHA).//P78723
- 15 F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.44:32:37//PSEUDOMONAS PUTIDA.//P25753
- 20 F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//5.0e-06:102:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
- 25 F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00036:134:321/HOMO SAPIENS (HUMAN).//P10162
- F-PLACE1010628
- 25 F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-12:37:81//HOMO SAPIENS (HUMAN).//P39194
- 30 F-PLACE1010630
- F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:62:30//EUMECES SKILTONIANUS (WESTERN SKINK).//P28118
- 35 F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//1.0:95:30//DROSOPHILA PSEUDOBSCURA (FRUIT FLY).//Q24617
- 40 F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332
- 45 F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:117:62//HOMO SAPIENS (HUMAN).//O14628
- 50 F-PLACE1010714
- F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//1.1e-64:176:76//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532
- 55 F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.97:31:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612

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- 5 F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//3.8e-05:253:30//MUS MUSCULUS (MOUSE)//P05143
- 10 F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II//1.5e-14:175:25//CAENORHABDITIS ELEGANS//Q09217
- 15 F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP//1.3e-120:216:89//MUS MUSCULUS (MOUSE)//Q02614
- 20 F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN)//0.97:133:24//DROSOPHILA MELANOGASTER (FRUIT FLY)//P54623
- 25 F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC)//0.0060:111:31//ESCHERICHIA COLI//Q99390
- 30 F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI//0.82:44:29//BACILLUS SP. (STRAIN TB-90)//Q07415
- 35 F-PLACE1010811//CYTOCHROME C-551 (C551)//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS//P38587
- 40 F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN)//2.8e-09:90:34//HOMO SAPIENS (HUMAN)//P41208
- 45 F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH)//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH)//P55848
- 50 F-PLACE1010857//IG ALPHA-1 CHAIN C REGION//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GORILLA)//P20758
- 55 F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //1.2e-56:173:58//HOMO SAPIENS (HUMAN)//Q05481
- F-PLACE1010877//HEAT SHOCK PROTEIN 82//0.13:130:25//ZEA MAYS (MAIZE)//Q08277
- F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIII C INTERGENIC REGION//0.95:51:27//BACILLUS SUBTILIS//P54436
- F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.)//0.98:71:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36002
- F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840//1.0:42:30//HAEMOPHILUS INFLUENZAE//P44897
- F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB3//0.060:59:35//OVIS

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ARIES (SHEEP).//P02444

5 F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN)  
(PEPLOMER PROTEIN).//0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191

10 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS TENAX  
VIRUS 1 (STRAIN KRA1) (TTV1).//P19285

F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.011:51:  
45//HOMO SAPIENS (HUMAN).//Q92558

15 F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE  
15 (PROTEIN EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567

20 F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17:71:  
38//BOS TAURUS (BOVINE).//P41987

F-PLACE1010947

25 F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:144:  
26//HOMO SAPIENS (HUMAN).//P09493

30 F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1 e-60:136:52//DROSOPHILA  
MELANOGASTER (FRUIT FLY).//P45890

F-PLACE1010965

35 F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA  
ANANASSAE (FRUIT FLY).//Q03293

40 F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H)  
(RNASE H).//1.0:32:37//SALMONELLA TYPHIMURIUM.//P23329

45 F-PLACE1011041//HOMEBOX PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS  
ELEGANS.//Q93899

50 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE  
PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1)  
(PLC-I) (PLC-154).//1.3e-22:58:93//RATTUS NORVEGICUS (RAT).//P10687

F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-07:38:73//HOMO  
SAPIENS (HUMAN).//P39195

55 F-PLACE1011056//HISTONE H1.//2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA).//P08283

F-PLACE1011057



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- 5 F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC  
REGION.//1.8e-07:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892
- 10 F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)  
//5.4e-25:63:88//RATTUS NORVEGICUS (RAT).//Q07803
- 15 F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:157:  
45//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09916
- 15 F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-  
GLYCOPROTEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743
- 20 F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS  
TYPE31.//P17385
- 25 F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.88:98:  
27//GLYCINE MAX (SOYBEAN).//Q02917
- 25 F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPARUM  
(ISOLATE FCM17 / SENEGAL).//P14586
- 30 F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.4e-13:98:50//HOMO  
SAPIENS (HUMAN).//P39188
- F-PLACE1011203
- 35 F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:48:27//EQUUS  
ASINUS (DONKEY).//P92479
- 40 F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-).//1.9e-15:162:  
31//STREPTOMYCES ANTIBIOTICUS.//Q03326
- F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (ISOLATE  
HP-438[MUNICH]).//P14369
- 45 F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15)  
(UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4)  
(DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:  
50 218:68//HOMO SAPIENS (HUMAN).//Q13107
- F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)  
(FRAGMENT).//3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485
- 55 F-PLACE1011273

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F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS)  
./0.011:36:50//RATTUS NORVEGICUS (RAT).//P20468

5 F-PLACE1011296//HOMEBOX PROTEIN DLX-6./0.76:55:32//BRACHYDANIO RERIO  
(ZEBRAFISH) (ZEBRA DANIO).//Q98877

10 F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-  
BINDING PROTEIN)./0.46:43:44//PETUNIA SP. (PETUNIA).//Q07060

15 F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME  
I./0.00021:171:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10411

F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101  
PRECURSOR./7.3e-27:113:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q05211

20 F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-07:40:62//HOMO  
SAPIENS (HUMAN).//P39188

25 F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI  
HEAVY CHAIN H2)./2.2e-54:227:44//MUS MUSCULUS (MOUSE).//Q61703

30 F-PLACE1011375//PROBABLE E5 PROTEIN./0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE  
51.//P26553

F-PLACE1011399//HISTONE H2B-IV./0.19:129:27//VOLVOX CARTERI.//P16868

35 F-PLACE1011419

F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT)./3.4e-05:133:24//GALLUS  
GALLUS (CHICKEN).//P55879

40 F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG./3.9e-25:76:63//HOMO  
SAPIENS (HUMAN).//P08547

45 F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN)./0.97:36:  
41//HOMO SAPIENS (HUMAN).//Q92838

50 F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1)./0.084:55:30//HOMARUS AMERICANUS  
(AMERICAN LOBSTER).//P29499

55 F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER  
PROTEIN B) (S-LAYER PROTEIN 1)./0.028:129:34//CLOSTRIDIUM  
THERMOCELLUM.//Q06852

F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR  
PRECURSOR (CTPT)./2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER).//P52178

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- 5 F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC  
REGION (086).//0.66:32:40//ESCHERICHIA COLI.//P52102
- F-PLACE1011520
- 10 F-PLACE1011563//LORICRIN.//0.00023:112:39//HOMO SAPIENS (HUMAN).//P23490
- F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.2e-31:78:76//HOMO  
SAPIENS (HUMAN).//P39195
- 15 F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)  
./1.5e-32:45:86//HOMO SAPIENS (HUMAN).//Q05481
- 20 F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-  
CONOTOXIN-SENSITIVE N- TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).//0.26:81:  
37//HOMO SAPIENS (HUMAN).//Q00975
- 25 F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180.//0.00045:170:30//PSEUDORABIES  
VIRUS (STRAIN INDIANA-FUNKHAUSER /BECKER) (PRV).//P11675
- F-PLACE1011641
- 30 F-PLACE1011643//CUTICLE COLLAGEN 40.//1.0:128:32//CAENORHABDITIS  
ELEGANS.//P34804
- 35 F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-15:44:63//HOMO  
SAPIENS (HUMAN).//P39188
- F-PLACE1011649//HYPOTHETICAL PROTEIN F-215.//0.48:106:34//HUMAN ADENOVIRUS  
TYPE 2.//P03291
- 40 F-PLACE1011650
- 45 F-PLACE1011664//CROOKED NECK PROTEIN.//1.2e-79:201:68//DROSOPHILA  
MELANOGASTER (FRUIT FLY).//P17886
- 50 F-PLACE1011675//FERREDOXIN.//1.0:44:29//METHANOCOCCUS  
THERMOLITHOTROPHICUS.//P21305
- F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC  
REGION.//1.0:40:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53098
- 55 F-PLACE1011719//NEUROTOXIN TX2-6.//0.90:31:35//PHONEUTRIA NIGRIVENTER  
(BRAZILIAN ARMED SPIDER).//P29425

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F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//0.0065:125:25//RATTUS NORVEGICUS (RAT).//Q63083

5 F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMENT).//0.97:48:39//EUBLEPHARIS MACULARIUS.//P40654

F-PLACE1011749

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F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).//0.028:91:39//MUS MUSCULUS (MOUSE).//Q60925

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F-PLACE1011778

F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).//0.97:48:43//MUS MUSCULUS (MOUSE).//P20863

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F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0027:154:33//BOS TAURUS (BOVINE).//P23206

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F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP).//1.0:60:26//PROSTHECOCHLORIS AESTUARII.//P11741

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F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION.//0.99:34:35//ACTERIOPHAGE T4.//P39495

F-PLACE1011891//SMOOTHELIN.//0.018:122:31//HOMO SAPIENS (HUMAN).//P53814

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F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//6.3e-09:203:35//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

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F-PLACE1011922//CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).//0.067:37:48//MUS MUSCULUS (MOUSE).//P50715

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F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//1.5e-83:175:89//MUS MUSCULUS (MOUSE).//P53351

F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.50:46:41//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//Q02593

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F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-05:47:51//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

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F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).//0.98:83:31//PLASMODIUM FRAGILE.//P22622

F-PLACE1011995

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5 F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254.//0.032:62:33//HOMO SAPIENS (HUMAN).//Q92543

10 F-PLACE2000003//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.4e-18:63:73//HOMO SAPIENS (HUMAN).//P39193

15 F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.14:20:50//BOS TAURUS (BOVINE).//P20072

20 F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0045:176:30//MUS MUSCULUS (MOUSE).//P05143

25 F-PLACE2000011//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-25:57:78//HOMO SAPIENS (HUMAN).//P39194

30 F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.00013:237:27//CAENORHABDITIS ELEGANS.//Q09475

35 F-PLACE2000015//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-33:60:80//HOMO SAPIENS (HUMAN).//P39193

40 F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP).//1.0:83:31//HOMO SAPIENS (HUMAN).//P14207

45 F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).//0.99:103:26//GALLUS GALLUS (CHICKEN).//Q07496

50 F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.69:29:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642

55 F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-).//1.1e-05:74:41//STREPTOMYCES ANTIBIOTICUS.//Q03326

F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).//6.7e-18:191:35//HOMO SAPIENS (HUMAN).//Q02246

F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//4.7e-80:163:96//RATTUS NORVEGICUS (RAT).//P38650

F-PLACE2000047//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/6.4e-06:63:49//HOMO SAPIENS (HUMAN).//P39191

F-PLACE2000050//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.2e-22:74:64//HOMO

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SAPIENS (HUMAN).//P39192

F-PLACE2000061

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F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS PROTEIN B).//1.9e-06:108:37//BACILLUS SUBTILIS.//P26907

10

F-PLACE2000072//ZINC FINGER PROTEIN 165.//3.5e-34:175:49//HOMO SAPIENS (HUMAN).//P49910

15

F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).//0.36:39:38//ONDATA ZIBETHICUS (MUSKRAT).//P00681

F-PLACE2000100

20

F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS).//0.18:32:37//ZEA MAYS (MAIZE).//P33626

25

F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR.//0.056:107:27//HOMO SAPIENS (HUMAN).//Q08708

30

F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT).//1.0:21:52//CLOSTRIDIUM PERFRINGENS.//Q46185

F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.4e-37:108:68//HOMO SAPIENS (HUMAN).//P39194

35

F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85.//0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03224

40

F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEPTOR) (PACAP-R-3).//0.83:65:32//MUS MUSCULUS (MOUSE).//P41588

45

F-PLACE2000140

F-PLACE2000164//TIPD PROTEIN.//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//O15736

50

F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERIOCIN B1).//1.0:30:26//CARNOBACTERIUM PISCICOLA.//P38579

55

F-PLACE2000172

F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526.//0.76:44:43//ARCHAEOGLOBUS

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FULGIDUS.//O29724

5 F-PLACE2000187//EM-LIKE PROTEIN GEA6.//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q02973

F-PLACE2000216

10 F-PLACE2000223//NEUROTOXIN III (LQQ III).//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01487

F-PLACE2000235

15 F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//5.1e-37:121:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

20 F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.4e-05:77:42//HOMO SAPIENS (HUMAN).//P39191

25 F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-46:232:45//TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN).//P23098

F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RABBIT).//P37709

30 F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.3e-06:33:66//HOMO SAPIENS (HUMAN).//P39188

35 F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45:33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329

40 F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.9e-08:35:71//HOMO SAPIENS (HUMAN).//P39195

45 F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.014:141:24//ORYCTOLAGUS CUNICULUS (RABBIT).//P11170

50 F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//5.7e-09:96:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

55 F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:49:53//HOMO SAPIENS (HUMAN).//Q13360

F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.5e-10:69:52//HOMO SAPIENS (HUMAN).//P39194

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- F-PLACE2000366
- 5 F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY  
PROTEIN)//1.5e-05:216:29//HOMO SAPIENS (HUMAN)//P54259
- 10 F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)  
//0.27:63:33//HOMO SAPIENS (HUMAN)//Q99583
- 15 F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN//0.72:120:31//EQUINE  
HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)//P28978
- F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.95:40:42//HOMO SAPIENS  
(HUMAN)//P02811
- 20 F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-)//0.88:88:31//AEROMONAS  
HYDROPHILA//Q07465
- 25 F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN)  
(CD99) (MIC2 PROTEIN) (12E7)//7.6e-16:180:39//HOMO SAPIENS (HUMAN)//P14209
- 30 F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA  
LIGASE) (LEURS)//1.7e-94:243:64//CAENORHABDITIS ELEGANS//Q09996
- 35 F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5)  
(PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT)//1.2e-09:78:39//MUS MUSCULUS  
(MOUSE)//Q60676
- F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-20:61:62//HOMO  
SAPIENS (HUMAN)//P39188
- 40 F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC  
REGION//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53211
- 45 F-PLACE2000427//INSULIN PRECURSOR//0.98:55:34//CERCOPITHECUS AETHIOPS  
(GREEN MONKEY) (GRIVET)//P30407
- 50 F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-07:65:50//HOMO  
SAPIENS (HUMAN)//P39188
- F-PLACE2000435
- 55 F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III//4.7e-  
66:178:47//CAENORHABDITIS ELEGANS//P34678
- F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.1e-23:88:62//HOMO



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SAPIENS (HUMAN).//P39195

5 F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT).//0.093:18:44//CENTRUROIDES  
LIMPIDUS LIMPIDUS (MEXICAN SCORPION).//P45630

10 F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT  
PROTEIN).//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450

F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.6e-23:73:63//HOMO  
SAPIENS (HUMAN).//P39188

15 F-PLACE2000477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-37:90:78//HOMO  
SAPIENS (HUMAN).//P39194

20 F-PLACE3000004//EYES ABSENT HOMOLOG 3.//1.1e-09:27:100//MUS MUSCULUS  
(MOUSE).//P97480

25 F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6.//0.0061:148:  
34//CAENORHABDITIS ELEGANS.//Q09457

30 F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III) (ATP  
PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//8.8e-93:193:92//RATTUS NORVEGICUS  
(RAT).//P21932

F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E.//0.15:50:38//METHANOCOCCUS  
JANNASCHII.//P54009

35 F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A.//0.96:50:34//BOS TAURUS (BOVINE)  
.//P48427

40 F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.29:22:  
59//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

45 F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE).//0.99:53:32//BACTERIOPHAGE  
ALPHA-3.//P31280

F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.4e-41:87:78//HOMO  
SAPIENS (HUMAN).//P39189

50 F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC151/1.0e-07:269:  
22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22224

55 F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.2e-29:97:73//HOMO  
SAPIENS (HUMAN).//P39188

F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1).//0.77:26:

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42//LOCUSTA MIGRATORIA (MIGRATORY LOCUST)//P80059

5 F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD2 3'REGION (ORF 63)//0.82:34:  
41//MARCHANTIA POLYMORPHA (LIVERWORT)//P38468

F-PLACE3000145//TENSIN//3.5e-91:238:74//GALLUS GALLUS (CHICKEN)//Q04205

10 F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-30:61:65//HOMO  
SAPIENS (HUMAN)//P39194

15 F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE  
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//1.4e-18:226:34//GIBBON APE  
LEUKEMIA VIRUS//P21414

20 F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.00014:  
107:33//ZEA MAYS (MAIZE)//P14918

25 F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE  
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//2.7e-19:169:30//BABOON  
ENDOGENOUS VIRUS (STRAIN M7)//P10272

30 F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC  
2.7.1.-)//0.0061:92:30//MYCOBACTERIUM TUBERCULOSIS//Q11053

F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.7e-49:56:80//HOMO  
SAPIENS (HUMAN)//P39189

35 F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR)  
(PROTEIN SXY)//0.39:94:34//HAEMOPHILUS INFLUENZAE//P43779

40 F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.6e-28:99:59//HOMO  
SAPIENS (HUMAN)//P39193

45 F-PLACE3000194//PROLINE-RICH PROTEIN LAS17//0.91:80:36//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST)//Q12446

F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT  
PROTEIN) (NF-M)//0.24:119:32//GALLUS GALLUS (CHICKEN)//P16053

50 F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH  
GLYCOPROTEIN)//0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

55 F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.5e-09:32:78//HOMO  
SAPIENS (HUMAN)//P39188

F-PLACE3000208

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F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-34:96:70//HOMO  
 SAPIENS (HUMAN).//P39194  
 5  
 F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING  
 PROTEIN) (BONE GLA- PROTEIN) (BGP).//0.46:13:53//CANIS FAMILIARIS (DOG).//P81455  
 10  
 F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-24:178:45//HOMO  
 SAPIENS (HUMAN).//P39188  
 F-PLACE3000226//30S RIBOSOMAL PROTEIN S18.//0.98:38:34//NEISSERIA  
 15 GONORRHOEAE.//O07815  
 F-PLACE3000230//METALLOTHIONEIN (MT).//0.97:25:48//OREOCHROMIS MOSSAMBICUS  
 (MOZAMBIQUE TILAPIA) (TILAPIA MOSSAMBICA).//P52726  
 20  
 F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).//8.0e-21:121:  
 39//HOMO SAPIENS (HUMAN).//P43361  
 25  
 F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//2.3e-125:264:  
 87//MUS MUSCULUS (MOUSE).//P53995  
 F-PLACE3000254//RTOA PROTEIN (RATIO-A).//0.99:142:23//DICTYOSTELIUM DISCOIDEUM  
 30 (SLIME MOLD).//P54681  
 F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-12:63:53//HOMO  
 SAPIENS (HUMAN).//P39188  
 35  
 F-PLACE3000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL  
 COLLAGEN).//1.0:55:38//HOMO SAPIENS (HUMAN).//P27658  
 40  
 F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//0.0028:31:54//HOMO SAPIENS (HUMAN).//P30808  
 F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY  
 45 PROTEIN).//0.98:82:34//RATTUS NORVEGICUS (RAT).//P54258  
 F-PLACE3000320  
 50  
 F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1  
 PRECURSOR.//2.2e-22:61:52//ORYZA SATIVA (RICE).//P25074  
 F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.32:15:  
 55 53//HOMO SAPIENS (HUMAN).//P22532  
 F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FRUIT FLY)

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//P24516

5 F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3)  
(FRAGMENT)//1.0:47:38//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL)//P24968

10 F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-)//3.9e-50:168:  
60//CAENORHABDITIS ELEGANS //P46549

F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.8e-29:76:71//HOMO  
SAPIENS (HUMAN)//P39194

15 F-PLACE3000353//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC  
2.4.1.41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:  
POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)//3.0e-09:100:  
41//HOMO SAPIENS (HUMAN)//Q10472

20 F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064//1.0:75:26//TREPONEMA  
PALLIDUM//O83103

25 F-PLACE3000363//METALLOTHIONEIN (MT)//0.067:42:33//ASTACUS FLUVIATILIS (BROAD-  
FINGERED CRAYFISH) (ASTACUS ASTACUS)//P55951

30 F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE)//1.0:65:27//BACTERIOPHAGE PHI-  
K//Q38040

35 F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPROTEIN//1.5e-18:90:47//HOMO  
SAPIENS (HUMAN)//P10267

F-PLACE3000388

40 F-PLACE3000399//!!!!ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.3e-45:60:75//HOMO  
SAPIENS (HUMAN)//P39193

F-PLACE3000400

45 F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.6e-09:46:73//HOMO  
SAPIENS (HUMAN)//P39188

50 F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.036:43:44//HOMO SAPIENS  
(HUMAN)//P39188

55 F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE//0.70:25:40//BOS TAURUS (BOVINE)  
//P01154

F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-09:49:67//HOMO  
SAPIENS (HUMAN)//P39195

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- 5 F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPHILA  
MELANOGASTER (FRUIT FLY).//P08175
- F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.67:236:21//BOS  
TAURUS (BOVINE).//P35662
- 10 F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:19:42//HOMO SAPIENS (HUMAN)  
.//P02814
- 15 F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS  
(BOVINE).//P02817
- 20 F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.//1.0:53:32//TACHYPLEUS  
TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P81281
- F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:55:32//DENDROASPIS  
ANGUSTICEPS (EASTERN GREEN MAMBA).//P80970
- 25 F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC)  
(FRAGMENT).//7.0e-19:180:27//HOMO SAPIENS (HUMAN).//P35749
- 30 F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.2e-15:  
193:30//HOMO SAPIENS (HUMAN).//P46100
- 35 F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR.//0.0024:97:  
29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P22815
- F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-32:79:75//HOMO  
SAPIENS (HUMAN).//P39194
- 40 F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1.//2.2e-99:178:97//MUS  
MUSCULUS (MOUSE).//P41233
- 45 F-PLACE4000063//IMMEDIATE-EARLY PROTEIN.//0.0017:159:25//HERPESVIRUS SAIMIRI  
(STRAIN 11).//Q01042
- F-PLACE4000089
- 50 F-PLACE4000093
- F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-14:68:60//HOMO  
SAPIENS (HUMAN).//P39188
- 55 F-PLACE4000106//1A PROTEIN [CONTAINS: HELICASE; METHYLTRANSFERASE].//1.0:46:  
41//BROAD BEAN MOTTLE VIRUS.//Q00020

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F-PLACE4000128//HYPOTHETICAL PROTEIN E-115//0.00020:101:30//HUMAN  
 ADENOVIRUS TYPE 2//P03290  
 5  
 F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD  
 PANCORNULIN)//0.15:57:31//HOMO SAPIENS (HUMAN)//P22528  
 10 F-PLACE4000131  
 F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR//1.0:45:24//BACILLUS  
 SUBTILIS//P45453  
 15 F-PLACE4000156//ZINC FINGER PROTEIN 136//2.1e-88:194:59//HOMO SAPIENS (HUMAN)  
 //P52737  
 20 F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654)//0.083:148:26//HOMO  
 SAPIENS (HUMAN)//P52746  
 25 F-PLACE4000211//CALPHOTIN//0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY)  
 //Q02910  
 F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-05:20:85//HOMO  
 SAPIENS (HUMAN)//P39188  
 30 F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE  
 (EC 2.1.1.45) (DHFR-TS)//1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI//Q27783  
 35 F-PLACE4000233  
 F-PLACE4000247//METALLOTHIONEIN (MT)//1.0e-05:34:41//PLEURONCTES PLATESSA  
 (PLAICE)//P07216  
 40 F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN)//0.99:33:42//CAPRINE  
 ARTHRITIS ENCEPHALITIS VIRUS (CAEV)//P31834  
 45 F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB//0.42:24:45//DROSOPHILA  
 MELANOGASTER (FRUIT FLY)//Q01643  
 50 F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-)//3.5e-09:189:  
 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32639  
 F-PLACE4000261//PEREGRIN (BR140 PROTEIN)//5.0e-11:103:37//HOMO SAPIENS  
 (HUMAN)//P55201  
 55 F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.037:181:  
 25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25386

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- 5 F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21)//1.0:46:39//MUS MUSCULUS (MOUSE)//P70375
- 10 F-PLACE4000300//50S RIBOSOMAL PROTEIN L32//0.81:28:46//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//P80339
- 15 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN)//1.6e-29:44:93//HOMO SAPIENS (HUMAN)//P42345
- 20 F-PLACE4000323
- 25 F-PLACE4000326//PARATHYMOSIN//0.0018:54:48//HOMO SAPIENS (HUMAN)//P20962
- 30 F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT)//0.97:28:42//SUS SCROFA (PIG)//Q00968
- 35 F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI)//1.0:33:36//STOICHACTIS HELIANTHUS (CARRIBEAN SEA ANEMONE) (STICHODACTYLA HELIANTHUS)//P19651
- 40 F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.071:42:42//SORGHUM VULGARE (SORGHUM)//P24152
- 45 F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-16:54:77//HOMO SAPIENS (HUMAN)//P39193
- 50 F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR//0.25:21:52//HORDEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE) //P25877
- 55 F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) (FRAGMENT)//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS//Q05338
- F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-29:96:67//HOMO SAPIENS (HUMAN)//P39194
- F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.3e-18:41:73//HOMO SAPIENS (HUMAN)//P39188
- F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-)//5.4e-21:237:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32639
- F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5'REGION PRECURSOR//0.00081:210:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40442

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- 5 F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC  
TRANSCRIPTION FACTOR HBP1)//0.020:87:33//TRITICUM AESTIVUM (WHEAT)//P23922
- 10 F-PLACE4000465//METALLOTHIONEIN-IL (MT-1L) (MT1X)//0.20:18:38//HOMO SAPIENS  
(HUMAN)//P80297
- 15 F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-19:73:52//HOMO  
SAPIENS (HUMAN)//P39188
- 20 F-PLACE4000489
- 25 F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1)//0.17:130:30//MUS  
MUSCULUS (MOUSE)//Q03173
- 30 F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE  
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT)//3.0e-05:50:36//MUS  
MUSCULUS (MOUSE)//P10400
- 35 F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1  
PRECURSOR//1.8e-45:231:47//RATTUS NORVEGICUS (RAT)//Q07008
- 40 F-PLACE4000548//CYTOCHROME C-551 (C551)//0.96:50:34//ECTOTHIORHODOSPIRA  
HALOPHILA//P00122
- 45 F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC  
3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING  
PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN)//1.6e-28:223:  
36//DROSOPHILA MELANOGASTER (FRUIT FLY)//P55824
- 50 F-PLACE000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-  
140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3)  
(LECAM3)//9.7e-11:166:281//HOMO SAPIENS (HUMAN)//P16109
- 55 F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE  
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]/1.6e-17:134:35//GIBBON APE  
LEUKEMIA VIRUS//P21414
- F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R)//1.0:  
54:29//RATTUS NORVEGICUS (RAT)//P30969
- F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT  
PROTEIN P12; CORE SHELL PROTEIN P30]/2.6e-14:221:32//MOLONEY MURINE SARCOMA  
VIRUS (STRAIN TS110)//P32594
- F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC



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REGION.//0.65:37:40//ESCHERICHIA COLI.//P37910

5 F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT)  
//1.0:33:33//HOMO SAPIENS (HUMAN).//P17020

F-PLACE4000654

10 F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC  
REGION.//1.6e-07:161:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33313

15 F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4  
SUBUNIT).//7.4e-15:223:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O60100

20 F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-  
14-6).//0.0013:128:35//GALLUS GALLUS (CHICKEN).//Q98937

F-SKNMC1000046//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS  
ELEGANS.//P08124

25 F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-  
ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.2e-41:87:98//HOMO SAPIENS  
(HUMAN).//P17655

30 F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR  
ERBB KINASES).//0.0032:154:35//HOMO SAPIENS (HUMAN).//O14511

35 F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5)  
(PNP/PMP OXIDASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.//Q20939

40 F-THYRO1000026//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.0e-13:54:66//HOMO  
SAPIENS (HUMAN).//P39192

F-THYRO1000034//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS B VIRUS  
(SUBTYPE AYW).//P03163

45 F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52)  
(CAMBRIDGE PATHOLOGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS (CRAB  
EATING MACAQUE) (CYNOMOLGUS MONKEY).//P32763

50 F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//BOS TAURUS  
(BOVINE).//P79244

55 F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:133:36//ORGYIA  
PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:205:

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29//HOMO SAPIENS (HUMAN)//Q00872

F-THYRO1000085

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F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.063:  
59:33//HOMO SAPIENS (HUMAN)//P49901

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F-THYRO1000107

F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.0e-58:110:  
67//NYCTICEBUS COUCANG (SLOW LORIS)//P08548

15

F-THYRO1000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//2.6e-06:  
134:35//MUS MUSCULUS (MOUSE)//Q62203

20

F-THYRO1000124//TENECIN 3 PRECURSOR//0.047:76:35//TENEBRIO MOLITOR (YELLOW  
MEALWORM)//Q27270

25

F-THYRO1000129//FBROSIN (FRAGMENT)//0.35:43:34//MUS MUSCULUS (MOUSE)  
//Q60791

30

F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.7e-14:104:42//HOMO  
SAPIENS (HUMAN)//P39188

F-THYRO1000156

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F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.7e-20:71:71//HOMO  
SAPIENS (HUMAN)//P39189

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F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT  
ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD  
SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM  
CHAIN)//6.7e-88:216:76//MUS MUSCULUS (MOUSE)//P35585

45

F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.9e-24:72:77//HOMO  
SAPIENS (HUMAN)//P39192

F-THYRO1000187

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F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT//0.060:50:  
42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P52871

55

F-THYRO1000197

F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III//2.0e-  
06:88:35//CAENORHABDITIS ELEGANS//34379

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F-THYRO1000206

5 F-THYRO1000221

F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC  
REGION.//1.0:51:35//AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS  
10 (ACMNPV).//P41661

F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.4e-37:  
137:36//HOMO SAPIENS (HUMAN).//P51523

15 F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
//0.11:21:52//HOMO SAPIENS (HUMAN).//P30808

20 F-THYRO1000270//WDNM1 PROTEIN PRECURSOR.//0.40:52:32//MUS MUSCULUS  
(MOUSE).//Q62477

F-THYRO1000279//BETA CRYSTALLIN A4.//0.97:64:26//BOS TAURUS (BOVINE).//P11842

25 F-THYRO1000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL  
PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).//3.4e-48:142:  
42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10071

30 F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT)  
//0.87:35:45//MUS MUSCULUS (MOUSE).//P10755

35 F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME  
I.//0.00010:75:26//CAENORHABDITIS ELEGANS.//P90859

40 F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN;  
BETA-GRANIN; WE-14].//0.88:107:26//MUS MUSCULUS (MOUSE).//P26339

F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//4.6e-25:49:81//MUS MUSCULUS  
(MOUSE).//P17563

45 F-THYRO1000368//LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR.//1.0:  
136:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09101

50 F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT  
PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN  
SARCOMA VIRUS.//P03330

55 F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90:46:  
30//HALICHOERUS GRYPUS (GRAY SEAL).//P38592

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F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.00019:48:37//HOMO SAPIENS (HUMAN).//P22531

5 F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

10 F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67:31//STAPHYLOCOCCUS AUREUS.//P48860

15 F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997

F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61) .//0.31:34:44//CARNOBACTERIUM PISCICOLA.//P38578

20 F-THYRO1000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2,1e-31:94:72//HOMO SAPIENS (HUMAN).//P39194

25 F-THYRO1000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.9e-08:30:86//HOMO SAPIENS (HUMAN).//P39195

30 F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.93:98:27//GLYCINE MAX (SOYBEAN).//Q02917

F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e-51:198:50//MUS MUSCULUS (MOUSE).//P15533

35 F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS MELLIFERA (HONEYBEE).//P31504

40 F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8)(HUMAN HERPESVIRUS 4).//P03181

45 F-THYRO1000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0.47:58:37//GALLUS GALLUS (CHICKEN).//Q03352

F-THYRO1000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:64:42//RATTUS NORVEGICUS (RAT).//P02454

50 F-THYRO1000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//0.94:61:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39725

55 F-THYRO1000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q13247

F-THYRO1000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR

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- ICP34.5) //0.99:37:40//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10) //P37319
- 5 F-THYRO1000602//EAMZP30-47 PROTEIN (FRAGMENT) //0.88:61:34//EIMERIA ACERVULINA //P21959
- 10 F-THYRO1000605//SUPPRESSOR PROTEIN SRP40 //0.0016:116:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32583
- 15 F-THYRO1000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! //3.4e-33:88:78//HOMO SAPIENS (HUMAN) //P39194
- 20 F-THYRO1000637//METALLOTHIONEIN A (MT A) //1.0:23:43//SPARUS AURATA (GILT HEAD SEA BREEM) //P52727
- 25 F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN //0.99:26:46//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA) //O19925
- 30 F-THYRO1000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! //1.5e-49:116:69//HOMO SAPIENS (HUMAN) //P39189
- 35 F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P //3.7e-15:119:43//ESCHERICHIA COLI //Q47155
- 40 F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1 //1.0e-44:232:41//CHLAMYDOMONAS REINHARDTII //P46870
- 45 F-THYRO1000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! //2.1e-15:144:39//HOMO SAPIENS (HUMAN) //P39193
- 50 F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REGION //0.00033:84:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53129
- 55 F-THYRO1000699//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!! //0.97:20:85//HOMO SAPIENS (HUMAN) //P39192
- F-THYRO1000712//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //4.2e-10:69:59//HOMO SAPIENS (HUMAN) //P39188
- F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H] //4.6e-10:204:32//HOMO SAPIENS (HUMAN) //P04280
- F-THYRO1000734
- F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT) //1.8e-46:130:70//HOMO SAPIENS (HUMAN) //O43295

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5 F-THYRO1000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-  
SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY)//1.1e-06:95:31//RATTUS  
NORVEGICUS (RAT)//Q64686

10 F-THYRO1000777//CUTICLE COLLAGEN 2C (FRAGMENT)//0.0031:119:34//HAEMONCHUS  
CONTORTUS//P16252

F-THYRO1000783//MYOSIN IC HEAVY CHAIN//0.0014:121:37//ACANTHAMOEBA  
CASTELLANII (AMOEBA)//P10569

15 F-THYRO1000787//HUNCHBACK PROTEIN (FRAGMENT)//0.54:25:52//PHOLCUS  
PHALANGIODES//Q02031

20 F-THYRO1000793//PRE-MRNA SPLICING FACTOR PRP9//0.91:3 0:36//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST)//P19736

F-THYRO1000796

25 F-THYRO1000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION//0.081:  
31:38//HUMAN ADENOVIRUS TYPE 41//P23691

30 F-THYRO1000815//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.0e-30:81:70//HOMO  
SAPIENS (HUMAN)//P39195

35 F-THYRO1000829//NEUROTOXIN III (BOM III)//0.022:32:34//BUTHUS OCCITANUS  
MARDOCHEI (MOROCCAN SCORPION)//P13488

F-THYRO1000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGION  
(ORF 109)//0.98:25:44//BACTERIOPHAGE P22//P26750

40 F-THYRO1000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//7.3e-09:83:  
42//VOLVOX CARTERI//P21997

45 F-THYRO1000855//ANTIFREEZE PEPTIDE 4 PRECURSOR//1.0:54:  
35//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER)//P02734

50 F-THYRO1000865//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!/5.2e-17:66:57//HOMO  
SAPIENS (HUMAN)//P39188

F-THYRO1000895//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-12:58:62//HOMO  
SAPIENS (HUMAN)//P39189

55 F-THYRO1000916//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.0e-32:101:69//HOMO  
SAPIENS (HUMAN)//P39189

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F-THYRO1000926//NITROGEN FIXATION REGULATORY PROTEIN.//5.5e-05:108:27//KLEBSIELLA OXYTOCA.//P56267

5 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//3.9e-50:147:40//HOMO SAPIENS (HUMAN).//P32322

10 F-THYRO1000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE KINASE).//1.8e-31:136:56//CITROBACTER FREUNDII.//P45510

15 F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR.//1.0:35:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32580

20 F-THYRO1000975

F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//1.3e-20:96:51//CAENORHABDITIS ELEGANS.//Q11076

25 F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN.//0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25160

30 F-THYRO1000988

F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGION.//0.97:60:31//ESCHERICHIA COLI.//P36675

35 F-THYRO1001031//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.5e-18:56:66//HOMO SAPIENS (HUMAN).//P39195

40 F-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//5.0e-13:126:35//HOMO SAPIENS (HUMAN).//P31948

45 F-THYRO1001062//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.1e-35:97:79//HOMO SAPIENS (HUMAN).//P39194

F-THYRO1001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//6.4e-13:70:57//HOMO SAPIENS (HUMAN).//P39194

50 F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:219:63//HOMO SAPIENS (HUMAN).//P98168

55 F-THYRO1001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.00068:160:31//HOMO SAPIENS (HUMAN).//Q15427

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- F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I.//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263
- 5 F-THYRO1001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.3e-15:59:66//HOMO SAPIENS (HUMAN).//P39188
- 10 F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161
- 15 F-THYRO1001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.0e-29:81:71//HOMO SAPIENS (HUMAN).//P39194
- 20 F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIS (EC 1.9.3.1).//0.88:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P20610
- 25 F-THYRO1001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-24:91:68//HOMO SAPIENS (HUMAN).//P39192
- 30 F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:165:39//MUS MUSCULUS (MOUSE).//P08043
- 35 F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.67:42:42//HOMO SAPIENS (HUMAN).//P02811
- 40 F-THYRO1001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.9e-16:61:68//HOMO SAPIENS (HUMM).//P39194
- 45 F-THYRO1001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-36:50:84//HOMO SAPIENS (HUMAN).//P39193
- 50 F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62:126:30//STREPTOMYCES FRADIAE.//P20186
- 55 F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION.//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888
- F-THYRO1001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT).//1.0:31:38//LAMELLIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM).//P20413
- F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00042:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
- F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BOVINE).//P04258
- F-THYRO1001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.5e-20:74:64//HOMO



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SAPIENS (HUMAN).//P39188

5 F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS  
(STRAIN COPENHAGEN).//P21123

10 F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8).//0.94:61:  
36//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01404

F-THYRO1001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0025:23:73//HOMO  
SAPIENS (HUMAN).//P39188

15 F-THYRO1001365//MERSACIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN HIL-  
Y85/54728).//P43683

20 F-THYRO1001374//PROTEIN VLDL.//1.6e- 3:140:31//HELICOBACTER PYLORI  
(CAMPYLOBACTER PYLORI).//O05729

F-THYRO1001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.047:43:48//HOMO  
SAPIENS (HUMAN).//P39192

25 F-THYRO1001403

F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0068:26:  
30 42//HOMO SAPIENS (HUMAN).//P22531

F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.1e-81:97:  
35 83//MUS MUSCULUS (MOUSE).//O70503

F-THYRO1001411//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.9e-26:89:74//HOMO  
SAPIENS (HUMAN).//P39193

40 F-THYRO1001426//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-09:55:61//HOMO  
SAPIENS (HUMAN).//P39193

45 F-THYRO1001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4).//0.68:44:34//BOS TAURUS  
(BOVINE).//P46162

F-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN  
HEAVY CHAIN, TYPE B) (NMMHC-B).//3.8e-64:216:62//HOMO SAPIENS (HUMAN).//P35580

50 F-THYRO1001480//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.3e-29:88:75//HOMO  
SAPIENS (HUMAN).//P39194

55 F-THYRO1001487//HOMEBOX PROTEIN HOX-B4 (HOX-2.6).//0.99:59:37//MUS MUSCULUS  
(MOUSE).//P10284

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F-THYRO1001534//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.4e-14:40:82//HOMO SAPIENS (HUMAN)//P39194

5 F-THYRO1001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION//2.4e-07:142:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38892

10 F-THYRO1001541//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.98:26:61//HOMO SAPIENS (HUMAN)//P39195

F-THYRO1001559//PROTEIN Q300//2.6e-05:20:75//MUS MUSCULUS (MOUSE)//Q02722

15 F-THYRO1001570

F-THYRO1001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.033:71:36//MUS MUSCULUS (MOUSE)//P15265

20 F-THYRO1001584//SUPPRESSOR PROTEIN SRP40//2.1e-05:188:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

25 F-THYRO1001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) //6.1e-21:35:91//HOMO SAPIENS (HUMAN)//Q15404

30 F-THYRO1001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH//1.0:57:42//HAEMOPHILUS INFLUENZAE//P44843

F-THYRO1001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIB//1.0:34:38//BUNGARUS FASCIATUS (BANDED KRAIT)//P25660

35 F-THYRO1001617//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.0e-18:55:81//HOMO SAPIENS (HUMAN)//P39194

40 F-THYRO1001637//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00020:25:80//HOMO SAPIENS (HUMAN)//P39195

45 F-THYRO1001656//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.0091:54:42//MUS MUSCULUS (MOUSE)//P05142

F-THYRO1001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182)//0.033:77:35//ESCHERICHIA COLI//P09160

50 F-THYRO1001671//((2'-5')OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2'-5')OLIGO(A) SYNTHETASE 1) (2-5A SYNTHETASE 1) (P46/P41) (E18/E16)//4.3e-34:207:34//HOMO SAPIENS (HUMAN)//P00973

55 F-THYRO1001673//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.9e-08:49:65//HOMO SAPIENS (HUMAN)//P39194

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5 F-THYRO1001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENIC  
 REGION.//6.4e-16:134:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06053  
 F-THYRO1001706  
 10 F-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-27:191:  
 36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-THYRO1001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1)  
 (PROTEIN KINASE A INTERFERENCE PROTEIN).//0.0032:105:32//SACCHAROMYCES  
 15 CEREVISIAE (BAKER'S YEAST).//P36027  
 F-THYRO1001745  
 20 F-THYRO1001746//GENE 10 PROTEIN.//1.0:55:30//SPIROPLASMA VIRUS SPV1-R8A2  
 B.//P15901  
 F-THYRO1001772//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.2e-05:41:63//HOMO  
 25 SAPIENS (HUMAN).//P39188  
 F-THYRO1001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III.//1.5e-  
 26:161:42//CAENORHABDITIS ELEGANS.//P41880  
 30 F-THYRO1001809//LATENCY-RELATED PROTEIN 2.//0.49:74:27//HERPES SIMPLEX VIRUS  
 (TYPE 1 / STRAIN F).//P17589  
 35 F-THYRO1001828//PROTEINASE INHIBITOR.//0.11:34:50//SOLANUM MELONGENA  
 (EGGPLANT) (AUBERGINE).//P01078  
 F-THYRO1001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING  
 40 INHIBITOR HOMOLOG) (DBI).//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG) (MARSH  
 FROG).//P45883  
 F-THYRO1001895//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.1e-09:72:47//HOMO  
 45 SAPIENS (HUMAN).//P39188  
 F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF)  
 (FRAGMENT).//0.79:36:44//TRYPANOSOMA CRUZI.//Q26327  
 50 F-VESEN1000122//HOMEBOX PROTEIN HB9.//0.57:64:32//HOMO SAPIENS (HUMAN)  
 .//P50219  
 55 F-Y79AA1000013//METALLOTHIONEIN B (MT-B).//0.034:35:48//SALMO SALAR (ATLANTIC  
 SALMON).//P52720

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- F-Y79AA1000033//CHOLECYSTOKININ.//0.97:49:30//PSEUDEMYS SCRIPTA (SLIDER TURTLE).//P80345
- 5 F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//1.4e-23:80:60//HOMO SAPIENS (HUMAN).//P35226
- 10 F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.0075:127:36//STREPTOMYCES FRADIAE.//P20186
- 15 F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.022:135:29//HOMO SAPIENS (HUMAN).//P10162
- F-Y79AA1000131//REGULATORY PROTEIN E2.//1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24.//P50770
- 20 F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.4e-06:187:29//MUS MUSCULUS (MOUSE).//P05143
- 25 F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//6.2e-09:47:53//OWENIA FUSIFORMIS.//P21260
- 30 F-Y79AA1000214//HISTONE H2A VARIANT.//1.7e-50:107:100//GALLUS GALLUS (CHICKEN).//P02272
- 35 F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I).//0.27:64:34//HOMO SAPIENS (HUMAN).//P01148
- 40 F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12.//2.5e-72:277:53//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O04658
- 45 F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.8e-08:174:35//MUS MUSCULUS (MOUSE).//P05142
- 50 F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.00020:176:33//RATTUS NORVEGICUS (RAT).//P13941
- 55 F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III.//0.092:127:21//CAENORHABDITIS ELEGANS.//Q09260
- F-Y79AA1000328//SEL-10 PROTEIN.//5.3e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794
- F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//1.0:73:30//OVIS ARIES (SHEEP).//P26372

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- F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)  
./1.8e-95:205:83//BOS TAURUS (BOVINE).//P53620
- 5 F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.036:37:  
54//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734
- 10 F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME  
III.//0.0031:106:28//CAENORHABDITIS ELEGANS.//Q10120
- 15 F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.4e-16:208:  
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343
- 20 F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA  
PIGMENT PROTEIN, ALPHA CHAIN C) (LH II-C ALPHA).//0.98:50:30//RHODOPSEUDOMONAS  
PALUSTRIS.//P35103
- 25 F-Y79AA1000410/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.9e-20:62:79//HOMO  
SAPIENS (HUMAN).//P39 194
- 25 F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC  
REGION.//1.4e-06:86:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53970
- 30 F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III.//2.8e-  
34:211:40//CAENORHABDITIS ELEGANS.//P34426
- 35 F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//3.9e-  
15:90:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414
- 40 F-Y79AA1000538/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.37:41:48//HOMO SAPIENS  
(HUMAN).//P39195
- 40 F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING  
FACTOR SRP75).//1.8e-21:190:37//HOMO SAPIENS (HUMAN).//Q08170
- 45 F-Y79AA1000540//SPERM PROTAMINE P1.//0.00045:66:45//DASYURUS VIVERRINUS  
(SOUTHEASTERN QUOLL), AND DASYURUS HALLUCATUS.//P42135
- 50 F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-  
C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR  
HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.6e-79:186:87//MUS MUSCULUS (MOUSE)  
./P17427
- 55 F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-) (FRAGMENT).//0.010:35:  
60//STREPTOMYCES PEUCETIUS.//P32009
- F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:197:

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36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P28320

5 F-Y79AA1000627//ZINC FINGER PROTEIN 134.//1.6e-34:191:35//HOMO SAPIENS (HUMAN)  
//P52741

10 F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC  
REGION.//8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P31380

F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A)  
//0.00037:108:27//CANDIDA BOIDINII (YEAST)//Q00316

15 F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//1.0e-  
23:210:34//CAENORHABDITIS ELEGANS//Q09316

20 F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X  
(HNRNP X) (CBP).//1.4e-53:156:68//MUS MUSCULUS (MOUSE)//Q61990

25 F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC  
REGION.//1.2e-11:231:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38205

F-Y79AA1000782//CUTICLE COLLAGEN 2.//0.012:56:35//CAENORHABDITIS  
ELEGANS//P17656

30 F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.3e-08:82:  
39//PLASMODIUM LOPHURAE//P04929

35 F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
//0.043:13:53//HOMO SAPIENS (HUMAN)//P30808

40 F-Y79AA1000800//PRIA PROTEIN PRECURSOR.//0.031:94:34//LENTINULA EDODES  
(SHIITAKE MUSHROOM) (LENTINUS EDODES)//Q01200

F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC  
REGION.//0.26:186:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53882

45 F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE).//0.99:78:  
35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P50998

50 F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC  
REGION.//3.4e-44:111:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48234

55 F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN.//0.0046:187:33//EPSTEIN-BARR  
VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//1.0e-75:239:66//CRICETULUS GRISEUS  
(CHINESE HAMSTER)//P05209

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- 5 F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.0078:57:31//HOMO SAPIENS (HUMAN)//P22532
- F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE//8.5e-11:241:26//GALLUS GALLUS (CHICKEN)//P10587
- 10 F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.69:122:31//TRYPANOSOMA BRUCEI BRUCEI//P24499
- 15 F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)//3.3e-102:211:93//RATTUS NORVEGICUS (RAT)//P70541
- F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:67:38//GALLUS GALLUS (CHICKEN)//P02457
- 20 F-Y79AA1000976//INVOLUCRIN//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN)//P24709
- 25 F-Y79AA1000985//PERICENTRIN//1.1e-24:116:59//MUS MUSCULUS (MOUSE)//P48725
- F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION//0.37:79:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38250
- 30 F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1]//0.93:43:39//SEPIA OFFICINALIS (COMMON CUTTLEFISH)//P80001
- 35 F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)//1.5e-51:211:52//BOS TAURUS (BOVINE)//P48818
- 40 F-Y79AA1001061//!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.8e-25:85:69//HOMO SAPIENS (HUMAN)//P39194
- F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]//0.0015:207:33//MUS MUSCULUS (MOUSE)//P28481
- 45 F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9)//0.99:36:41//ARANEUS DIADEMATUS (SPIDER)//P80515
- 50 F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III//1.0e-06:197:23//CAENORHABDITIS ELEGANS //P34492
- 55 F-Y79AA1001105//HOMEODOMAIN PROTEIN OTX2//2.9e-62:163:79//MUS MUSCULUS (MOUSE) //P80206
- F-Y79AA1001145//!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.024:42:59//HOMO

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SAPIENS (HUMAN).//P39195

5 F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC  
REGION.//0.96:20:50//AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS  
(ACMNPV).//P41471

10 F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BARR  
VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

15 F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:  
38//CAENORHABDITIS ELEGANS.//Q09456

F-Y79AA1001211

20 F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205

F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO  
SAPIENS (HUMAN).//Q02817

25 F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD  
1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS  
NORVEGICUS (RAT).//P51657

30 F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC  
REGION.//2.0e-22:108:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238

F-Y79AA1001281

35 F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS  
MUSCULUS (MOUSE).//P05143

40 F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:  
117:25//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P92959

45 F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-  
RICH SQUAMOUS CELL MARKER) (SPRP).//0.082:44:40//SUS SCROFA (PIG).//P35323

50 F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:47:40//MUS  
MUSCULUS (MOUSE).//P33622

F-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).//9.8e-58:157:62//HOMO  
SAPIENS (HUMAN).//P31271

55 F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q07283

F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS



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MUSCULUS (MOUSE).//P70459

5 F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44//CAENORHABDITIS ELEGANS.//Q11076

10 F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.3e-17:249:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313

F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I49 KD POLYPEPTIDE (EC 2.7.7.6) (A49).//0.0099:155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q01080

15 F-Y79AA1001541

20 F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-17:53:83//HOMO SAPIENS (HUMAN).//P39192

F-Y79AA1001555//MAJOR SURFACE ANTIGEN.//0.046:62:29//HEPATITIS B VIRUS.//P31873

25 F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//8.6e-11:144:31//ESCHERICHIA COLI.//P27550

30 F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.012:64:40//MUS MUSCULUS (MOUSE).//P15265

F-Y79AA1001594//CORNIFIN BETA.//0.61:88:31//MUS MUSCULUS (MOUSE).//O09116

35 F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.024:170:30//HOMO SAPIENS (HUMAN).//O00268

40 F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZFI-1).//4.5e-09:136:27//HOMO SAPIENS (HUMAN).//P28698

F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.093:94:26//MYCOBACTERIUM TUBERCULOSIS.//P71779

45 F-Y79AA1001665//HOMEBOX PROTEIN DLX-2 (HOMEBOX PROTEIN TES-1).//0.79:90:26//MUS MUSCULUS (MOUSE).//P40764

50 F-Y79AA1001679//LAMBDA-CRYSTALLIN.//1.6e-95:224:81//ORYCTOLAGUS CUNICULUS (RABBIT).//P14755

55 F-Y79AA1001692//GERM CELL-LESS PROTEIN.//3.5e-08:78:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820

F-Y79AA1001696//INSULIN.//1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL).//P42633

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- F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN./0.0013:192:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
- 5 F-Y79AA1001711//PARATHYMOSIN (ZINC-BINDING 11.5 KD PROTEIN)./0.032:38:34//RATTUS NORVEGICUS (RAT).//P04550
- F-Y79AA1001781
- 10 F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP)./0.0063:128:30//HOMO SAPIENS (HUMAN).//P50552
- 15 F-Y79AA1001827//SPERM PROTAMINE P1./0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305
- 20 F-Y79AA1001846//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!/2.4e-09:42:73//HOMO SAPIENS (HUMAN).//P39188
- F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT)./1.8e-10:63:44//PSYCHODA CINEREA//Q02035
- 25 F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)./0.00036:108:37//MUS MUSCULUS (MOUSE).//Q61967
- 30 F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN-1 RECEPTOR) (CD134 ANTIGEN)./3.2e-07:100:35//HOMO SAPIENS (HUMAN).//P43489
- 35 F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD)./0.020:25:64//HOMO SAPIENS (HUMAN).//P20931
- 40 F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)./0.016:83:36//HOMO SAPIENS (HUMAN).//P10162
- F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C./8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)./O42643
- 45 F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)./9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743
- 50 F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)./0.036:53:45//HOMO SAPIENS (HUMAN).//P30808
- 55 F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A9.4 IN CHROMOSOME III./0.12:

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171:22//CAENORHABDITIS ELEGANS.//P34384

5 F-Y79AA1002093//MAX PROTEIN.//3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFISH)  
(ZEBRA DANIO).//P52161

10 F-Y79AA1002103//SHORT NEUROTOXIN C.//0.040:21:47//AIPYSURUS LAEVIS (OLIVE SEA  
SNAKE).//P19958

F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827.//0.84:68:30//METHANOCOCCUS  
JANNASCHII.//Q58237

15 F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC  
REGION.//3.4e-29:197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206

20 F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//1.9e-19:120:45//DROSOPHILA  
MELANOGASTER (FRUIT FLY).//Q24133

F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6).//0.0011:162:32//MUS MUSCULUS  
(MOUSE).//P70327

25 F-Y79AA1002208//ANKYRIN.//2.9e-08:231:29//MUS MUSCULUS (MOUSE).//Q02357

30 F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC  
6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//3.7e-23:170:32//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P48527

35 F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK)  
.//0.0061:69:31//HOMO SAPIENS (HUMAN).//P35321

F-Y79AA1002211//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//9.2e-10:43:62//HOMO  
SAPIENS (HUMAN).//P39193

40 F-Y79AA1002220

45 F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME  
I.//1.9e-21:147:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264

F-Y79AA1002234

50 F-Y79AA1002246//MYOSIN IC HEAVY CHAIN.//0.00066:131:34//ACANTHAMOEBA  
CASTELLANII (AMOEBIA).//P10569

55 F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III.//4.3e-  
45:164:48//CAENORHABDITIS ELEGANS.//Q02328

F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS:

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PEPTIDE P-DJ (FRAGMENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161

F-Y79AA1002307

5

F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.75:198:24//CAENORHABDITIS ELEGANS.//P46012

10

F-Y79AA1002351//CUTICLE COLLAGEN 34.//0.74:128:35//CAENORHABDITIS ELEGANS.//P34687

15

F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2.//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40036

20

F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691

25

F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION.//3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53899

30

F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:162:84//HOMO SAPIENS (HUMAN).//P17812

35

F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.81:34:41//HOMO SAPIENS (HUMAN).//P22531

40

F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68.//0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558

45

F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).//P15620

50

F-Y79AA1002482//ZINC FINGER PROTEIN 141.//2.0e-31:90:55//HOMO SAPIENS (HUMAN).//Q15928

55

F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

Homology Search Result Data 2.

The result of the homology search of the GenBank using the clone sequence of 5'-end except

EST and STS.

Data include

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the name of clone,

definition of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.4e-106:695:86//L16953

F-HEMBA1000012//Caenorhabditis-elegans cosmid C16C10, complete sequence.//1.5e-24:374:66//Z46787

F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344

F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein (GIT1) mRNA, complete cds.//5.6e-124:743:88//AF085693

F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-25:529:65//AC004581

F-HEMBA1000046//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING DRAFT SEQUENCE.//3.2e-11:330:63//AL033528

F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence.//0.32:407:59//AL022477

F-HEMBA1000076//Homo sapiens full-length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182

F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 2291M18 genomic survey sequence.//2.8e-16:132:79//AQ004134

F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//8.6e-98:230:93//AC003104

F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340

F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:

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96//AB018331

5 F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete  
cds.//1.1e-10:409:60//AF056324

F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741

10 F-HEMBA1000168//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
321D2, WORKING DRAFT SEQUENCE.//0.99:290:61//AL031033

15 F-HEMBA1000180//rat u2 small nuclear rna gene and flanks.//3.7e-18:112:98//K00034

F-HEMBA1000185

20 F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:191:67//L19476

F-HEMBA1000201//Human Ini1 mRNA, complete cds.//2.0e-73:440:92//U04847

25 F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence.//0.90:332:  
59//AL034559

30 F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete  
cds.//4.8e-117:585:83//AF060194

F-HEMBA1000227//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179h6,  
reverse read cpg179h6.rt1a.//1.9e-14:95:98//Z64921

35 F-HEMBA1000231//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse  
read cpg90a5.rt1a.//5.1e-34:186:97//Z56144

40 F-HEMBA1000243//Human DNA sequence from PAC 440O21 on chromosome X contains  
ESTs and STS.//4.1e-67:291:82//Z84481

F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankydn.//0.029:316:59//X69065

45 F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete  
sequence.//0.35:467:60//AC004454

F-HEMBA1000264

50

F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2  
unordered pieces.//8.9e-20:218:78//AC004825

55 F-HEMBA1000282//Homo sapiens chromosome Y, clone 264,M,20, complete  
sequence.//4.2e-08:134:77//AC004617

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F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence.//1.1e-06:152:73//B17459

5 F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds.//3.2e-11:507:62//M33764

10 F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey sequence.//5.4e-06:86:88//B90730

F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.9e-111:701:86//AF030131

15 F-HEMBA1000304//HS\_3006\_A1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence.//5.2e-40:240:92//AQ118226

20 F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein.//7.9e-127:815:84//Y10495

25 F-HEMBA100 0327//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.4e-11:87:96//AQ187492

30 F-HEMBA1000333

F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence.//4.0e-66:271:84//AF031078

35 F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.64:334:60//AC004848

40 F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds.//0.017:313:63//J25056

F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.87:198:61//L40178

45 F-HEMBA1000357//HS\_3194\_A1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//6.5e-90:436:98//AQ173748

50 F-HEMBA1000366//HS\_3027\_B2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence.//0.0074:192:64//AQ128843

55 F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to

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monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587

5 F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.6e-22:659:63//AC006116

10 F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPCI11-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122

15 F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence.//3.5e-111:284:95//AC004520

F-HEMBA1000392//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL031984

20 F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//9.5e-35:364:73//U80460

25 F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409

30 F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584

F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112

35 F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554

40 F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393

F-HEMBA1000442

45 F-HEMBA1000456//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//6.3e-06:62:96//B85188

50 F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808

55 F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839

F-HEMBA1000464//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.8e-25:397:72//AC006213



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- 5 F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21,  
genomic survey sequence.//4.0e-83:406:99//B94160
- 10 F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT  
Region, complete sequence.//4.2e-53:312:93//AC004033
- 15 F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y13334
- F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-  
06:338:58//X00740
- 20 F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete  
sequence.//9.4e-41:591:69//AC005884
- F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:  
57:100//D13666
- 25 F-HEMBA1000505
- F-HEMBA1000508//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4,  
BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered  
pieces.//0.035:329:61//AC004661
- 30 F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642
- 35 F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC  
library) complete sequence.//1.6e-53:300:89//AC004616
- 40 F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//1.7e-10:117:86//AC006006
- F-HEMBA1000523
- 45 F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-  
35:290:80//U08215
- 50 F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177\_H\_5, WORKING  
DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973
- F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAI  
project).//0.057:265:63//AL033545
- 55 F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-  
110:572:88//D89340

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F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237

5 F-HEMBA1000555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134O19, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555

10 F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP, Homo sapiens genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611

15 F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564

F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC005504

20 F-HEMBA1000568//HS\_3243\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence.//3.1e-54:323:91//AQ219628

25 F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:61//X89571

30 F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//AC005506

F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//1.7e-11:132:79//AF045573

35 F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.3e-43:228:97//AJ007509

40 F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence.//7.3e-07:68:94//AF046733

45 F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//8.7e-71:553:79//Z83822

F-HEMBA1000604//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING DRAFT SEQUENCE.//2.9e-21:158:75//AL021394

50 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.1e-118:561:99//AB007925

55 F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//2.2e-28:426:70//AC004382

F-HEMBA1000636//Human CpG island sequence, clone Q28B8.//1.0e-15:274:68//D85773

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- 5 F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//6.7e-137:639:99//AB014590
- F-HEMBA1000655//, complete sequence.//5.1e-83:685:80//AC005815
- 10 F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.1e-91:597:84//U35776
- F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.019:695:57//AC004907
- 15 F-HEMBA1000673//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//1.5e-48:325:85//Z86090
- 20 F-HEMBA1000682//Homo sapiens (subclone 5\_g5 from P1 H25) DNA sequence.//7.7e-61:615:74//L43411
- F-HEMBA1000686
- 25 F-HEMBA1000702
- F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0037:569:57//AC005507
- 30 F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2.//2.0e-09:483:62//AL031124
- 35 F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome.//0.00058:762:57//U87145
- F-HEMBA1000726//H.sapiens HLA-DRB1\*15 gene.//9.8e-49:189:89//X88791
- 40 F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0054:206:67//B60158
- 45 F-HEMBA1000747
- F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.3e-05:124:75//AL024509
- 50 F-HEMBA1000752//Human Chromosome X, complete sequence.//5.9e-48:502:75//AC004073
- 55 F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5

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unordered pieces.//0.011:179:67//AC005043

5 F-HEMBA1000773//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
clone Y59A8, WORKING DRAFT SEQUENCE.//0.070:231:63//Z98870

10 F-HEMBA1000774//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete  
sequence.//6.2e-40:385:75//AC004953

F-HEMBA1000791

15 F-HEMBA1000817//Myrmecia pilosula HI87-135 mitochondrion cytochrome b gene, partial  
cds.//0.99:244:58//U15678

20 F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791  
and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG  
island.//0.033:294:62//Z81370

25 F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome.//9.7e-05:  
463:58//AE001164

30 F-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome  
20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-  
Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-  
Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable  
Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains  
a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//3.0e-153:732:  
98//AL022394

35 F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2  
mRNA, complete cds.//1.6e-31:386:72//AF059273

40 F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer  
Institute Human PAC Library) containing Arylsulfatase D and E genes, complete  
sequence.//8.5e-115:455:98//AC005295

45 F-HEMBA1000867

50 F-HEMBA1000869//Human DNA sequence from cosmid J138O17, between markers  
DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous  
retroviral like element.//6.6e-41:424:75//Z72519

55 F-HEMBA1000870//Gnamptodon pumilio cytochrome oxidase II gene, partial cds; and tRNA-  
Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for  
mitochondrial products.//0.0049:211:66//AF034598

F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 2355D20,

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genomic survey sequence.//3.7e-33:180:98//AQ059583

5 F-HEMBA1000876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//5.6e-37:262:72//Z83826

10 F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds.//1.0:304:59//AF015523

F-HEMBA1000910//M.musculus necdin mRNA, complete cds.//6.1e-08:256:61//M80840

15 F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region.//0.13:232:63//U88158

F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds.//1.0:213:65//U00147

20 F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence.//5.5e-11:275:64//B69224

25 F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces.//9.7e-05:78:83//AC004878

30 F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_15, complete sequence.//5.8e-140:661:99//AC005324

F-HEMBA1000946

35 F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12 unordered pieces.//8.3e-16:181:75//AC004967

40 F-HEMBA1000968//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 69M21, WORKING DRAFT SEQUENCE.//4.4e-117:398:86//AL031735

F-HEMBA1000971//H.sapiens CpG island DNA genomic Mse1 fragment, clone 182f4, forward read cpg182f4 ft1a.//1.5e-20:126:96//Z57528

45 F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11.//0.34:642:59//AB020858

50 F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//5.1e-183:865:98//AC004817

55 F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds.//0.00065:391:62//M30023

F-HEMBA10009851//Human DNA sequence from clone 272E8 on chromosome Xp22.13-

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22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.4e-05:243:65//Z93929

5 F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence.//6.6e-06:508:61//AD000813

10 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds.//1.2e-22:193:84//D84064 F-HEMBA1001007

15 F-HEMBA1001008//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//7.8e-46:532:73//AL031577

20 F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence.//0.97:369:59//X17115

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//4.4e-139:661:98//AB007937

25 F-HEMBA1001019//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//1.6e-16:521:64//AC006213

30 F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178\_C\_3, complete sequence.//3.8e-50:367:72//AC005702

F-HEMBA1001022

35 F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0e-23:378:69//AE000658

40 F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//7.6e-19:867:60//Z86064

45 F-HEMBA1001043//HS\_2219\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521

50 F-HEMBA1001051//Human Chromosome X clone bW XD342, complete sequence.//4.8e-79:308:84//AC004072

F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341

55 F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084

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F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855\_D\_21 complete sequence.//0.98:280:62//AC006079

5 F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal propeptide.//1.1e-31:181:96//X01742

10 F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt].//3.6e-13:338:65//S78219

F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446

15 F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase llx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586

20 F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I25863

F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105

25 F-HEMBA1001099

30 F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence.//2.4e-58:347:87//AC005250

F-HEMBA1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723

35 F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383

40 F-HEMBA1001123//Homo sapiens full-length insert cDNA clone ZD38E12.//1.1e-11:231:68//AF086247

45 F-HEMBA1001133//Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909

F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds.//6.9e-72:527:77//AB018341

50 F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077

55 F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507

F-HEMBA1001174//R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-

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59:565:73//X78604

5 F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815

10 F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410

F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917

15 F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009

20 F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601\_N\_13, complete sequence.//0.0086:372:58//AC005389

25 F-HEMBA1001247//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b11, reverse read cpg11b11.rt1a.//2.0e-24:154:93//Z64441

F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:659:81//AF047020

30 F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205

F-HEMBA1001281

35 F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:236:81//X15543

40 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.5e-28:530:64//AC004131

F-HEMBA1001294//Yeast mitochondrial aapl gene for ATPase subunit 8.//2.8e-15:722:60//X00960

45 F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003

50 F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260

55 F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505

F-HEMBA1001310//HS\_3252\_B2\_B12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey sequence.//1.2e-



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16:166:82//AQ217054

5 F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6,  
genomic survey sequence.//0.33:256:59//B79408

10 F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.//7.8e-30:  
165:99//L20861

15 F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6.  
Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase  
LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-  
phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains  
ESTs, GSSs(BAC end sequences) and a CA repeat polymorphism, complete  
sequence.//5.4e-19:347:68//AL021368

20 F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10,  
genomic survey sequence.//0.012:152:65//AQ075713

25 F-HEMBA1001330//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
contig 3-103, complete sequence.//0.0037:254:62//AL010208

30 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA,  
complete cds.//1.1e-103:516:97//AF057358

F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete  
sequence.//1.7e-150:706:99//AC006241

35 F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL033505

40 F-HEMBA1001377//HS\_3020\_B1\_D12\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey  
sequence.//0.00022:63:77//AQ105297

45 F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of the complete  
sequence.//0.00035:317:60//AE001431

50 F-HEMBA1001387//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-  
90:437:98//AQ155035

F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15  
unordered pieces.//4.2e-47:159:89//AC005073

55 F-HEMBA1001391//Human DNA sequence from clone 409O10 on chromosome 20q12  
Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031256

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F-HEMBA1001398//H.sapiens CpG island DNA genomic Mse1 fragment, clone 70d11,  
forward read cpg70d11.ft1b//0.018:46:97//Z62591

5 F-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380

10 F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:  
57//U03645

15 F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic  
survey sequence.//8.4e-12:516:60//AG001050

F-HEMBA1001413

20 F-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
41018, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732

25 F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//8.0e-177:859:97//AC006146

F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:  
64//AC004917

30 F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete  
sequence.//1.2e-74:284:84//AC005670

35 F-HEMBA1001442//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
contig 3-66, complete sequence.//0.056:194:63//AL010138

40 F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete  
sequence.//0.96:328:61//AC004047

F-HEMBA1001450

45 F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-  
11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB, ESTs and STS, complete  
sequence.//2.0e-47:468:73//AL031115

50 F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2,  
genomic survey sequence.//1.5e-05:223:65//B78859

55 F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo  
sapiens genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652

F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:  
99//AB011144

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- 5 F-HEMBA1001478//HS\_2228\_A2\_B03\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-  
40:275:88//AQ032041
- 10 F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3.  
Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and  
another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene).  
Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete  
sequence.//7.7e-47:311:85//AL031133
- 15 F-HEMBA1001510//Human HLA class III region containing cAMP response element binding  
protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds,  
complete sequence.//2.0e-130:699:93//U89337
- 20 F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete  
sequence.//4.1e-114:711:85//AC005794
- 25 F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete  
sequence.//5.7e-162:769:98//AC004549
- F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328.//8.6e-17:498:61//U50193
- 30 F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of  
the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands,  
//0.31:120:69//Z98258
- 35 F-HEMBA1001533
- F-HEMBA1001557//Chionoecetes opilio (clone COP41) DNA microsatellite repeat  
regions.//7.0e-25:303:72//L49136
- 40 F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-  
25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-  
containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8,  
45 Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-  
containing Monooxygenase family protein. Contains ESTs and GSSs, complete  
sequence.//7.2e-18:805:60//AL021026
- 50 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2  
(VAMP2).//1.1e-64:338:95//AJ225044
- 55 F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete  
sequence.//2.1e-148:698:99//AC004453
- F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:

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99//AJ012449

5 F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980

F-HEMBA1001585

10 F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432

15 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918

F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131

20 F-HEMBA1001620//Oryza sativa RINO1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107

25 F-HEMBA1001635//HS\_3208\_A1\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944

30 F-HEMBA1001636//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216

35 F-HEMBA1001640//HS\_3253\_B2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058

F-HEMBA1001647//H.sapiens gene for plectin.//0.00052:629:61//Z54367

40 F-HEMBA1001651//Salmo salar DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206

45 F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368

F-HEMBA1001658//M.musculus COL3A1 gene for collagen alpha-I.//2.4e-30:742:62//X52046

50 F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740

55 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247

F-HEMBA1001675//RPCI11-54F8.TV RPCI11 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126

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F-HEMBA1001678//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//AC002349

5

F-HEMBA1001681

F-HEMBA1001702//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398

10

F-HEMBA1001709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531

15

F-HEMBA1001711//Lysiphlebus melandriicola NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178

20

F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete sequence.//0.091:315:61//AC004519

25

F-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250

30

F-HEMBA1001718//HS\_3056\_A2\_H08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=O, genomic survey sequence.//2.0e-79:383:99//AQ106367

35

F-HEMBA1001723//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793

40

F-HEMBA1001731//HS\_3021\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658

45

F-HEMBA1001734//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.00060:392:60//AC004617

50

F-HEMBA1001744//HS\_3194\_A1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295

55

F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//AC002102

F-HEMBA1001746//HS\_2163\_B1\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995

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- 5 F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//AC002109
- F-HEMBA1001781
- 10 F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered-pieces.//5.5e-13:296:65//AC002099
- 15 F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038458
- F-HEMBA1001800//CrT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//2.2e-40:335:80//AQ009222
- 20 F-HEMBA1001803//M.musculus (Ba1b/C) P/L01 mRNA.//1.7e-25:286:74//Z31360
- F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977
- 25 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98//AB007969
- 30 F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:639:57//AJ004801
- F-HEMBA1001815
- 35 F-HEMBA1001819//HS\_3079\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616
- 40 F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60//AC005013
- 45 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243
- F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:344:68//AF020275
- 50 F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58//AC005161
- 55 F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//1.2e-22:316:70//AC005867
- F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126

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- 5 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517
- 10 F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.//0.38:337:62//AC005395
- 15 F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735
- 20 F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//6.7e-98:288:91//AC005065
- 25 F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476:84//AC003693
- 30 F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF026954
- 35 F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63//AC003065
- 40 F-HEMBA1001912//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732
- 45 F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219:65//AC005766
- 50 F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer , segment 5/10.//0.00011:366:63//AB020873
- 55 F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031
- 60 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145
- 65 F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310
- 70 F-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629

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F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//0.097:107:71//AC006057

5 F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934

10 F-HEMBA1001950//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, forward read cpg15b5.f1q.//1.4e-27:168:95//Z54728

15 F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390

F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507

20 F-HEMBA1001964

25 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178

30 F-HEMBA1001979//HS\_3067\_B1\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506

35 F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551

40 F-HEMBA1001991//HS\_2237\_A2\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283

45 F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449

F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948

50 F-HEMBA1002018

F-HEMBA10020227//Human p37NB mRNA, complete cds.//0.014:58:96//U32907

55 F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284

F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3.



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Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053

- 5 F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-42:532:63//AC005216
- 10 F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//0.81:435:59//AF025422
- 15 F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:769:87//U92703
- F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943
- 20 F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//D83649
- 25 F-HEMBA1002113//F.rubripes GSS sequence, clone 063K10bB4, genomic survey sequence.//0.029:142:66//Z88840
- F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.3e-14:515:62//AC000378
- 30 F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds.//0.98:222:61//AF031815
- 35 F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence.//0.0081:371:60//Z81549
- 40 F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA-Met (tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888
- F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263
- 45 F-HEMBA1002151
- 50 F-HEMBA1002153//CITBI-E1-2519120.TR CITBI-E1 Homo sapiens genomic clone 2519120, genomic survey sequence.//8.5e-61:334:94//AQ277613
- F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232
- 55 F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//AF006829

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- 5 F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210
- 10 F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712
- 15 F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000066
- 20 F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00066:466:59//AC004825
- 25 F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-23:176:77//AC005015
- 30 F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589
- 35 F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence.//1.8e-20:368:66//AC005150
- 40 F-HEMBA1002204//HS\_2055\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=O, genomic survey sequence.//1.2e-06:178:65//AQ235350
- 45 F-HEMBA1002212//S.cerevisiae chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149
- 50 F-HEMBA1002215//M.musculus mRNA for testin.//4.6e-80:504:87//X78989
- 55 F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-63:336:74//AC003035
- F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//2.6e-39:311:81//AC006044
- F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//1.6e-12:397:64//AC004861
- F-HEMBA1002241
- F-HEMBA1002253
- F-HEMBA1002257//Homo sapiens diacylglycerol kinase .iota (DGKi) mRNA, complete

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cds.//3.5e-151:731:97//AF061936

5 F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-  
qter contains ESTs, STS and endogenous retrovirus.//1.3e-09:313:62//Z71183

F-HEMBA1002267

10 F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human  
BAC Library) complete sequence.//0.069:495:58//AC006210

15 F-HEMBA1002321//Homo sapiens PAC clone DJ0991O23, complete sequence.//0.019:564:  
58//AC004944

20 F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone  
2387N15, genomic survey sequence.//1.8e-71:346:99//AQ240836

F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8,  
complete sequence.//0.84:547:57//AB020754

25 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-185:872:  
98//AB018314

30 F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24,  
genomic survey sequence.//9.1e-33:230:75//AQ110676

35 F-HEMBA1002349//Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete  
cds.//9.4e-06:504:57//J69551

F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA,  
complete cds.//7.3e-188:872:99//AF092563

40 F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of  
hepatocellular colorectal and non-small cell lung cancer , segment 11/11.//2.1e-20:262:  
72//AB020868

45 F-HEMBA1002389//D.discoideum spore coat 60 (sp60) gene, 5' flank.//0.010:95:73//M34546

50 F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds.//6.2e-120:767:  
85//AF023617

55 F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library C Homo  
sapiens genomic clone Plate=CT 830 Col=1 Row=K, genomic survey sequence.//7.6e-06:  
111:76//B38165

F-HEMBA1002430//HS\_3137\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence.//1.6e-

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56:367:88//AQ148697

- 5 F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.67:129:64//M25216
- F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds.//1.1e-30:274:72//AF051347
- 10 F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-173:822:98//AC005378
- F-HEMBA1002462//Sequence 41 from patent US 5708157.//9.8e-51:519:73//I80067
- 15 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds.//4.0e-108:603:92//D50912
- F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4.//0.0068:626:57//AL031514
- 20 F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//1.5e-40:349:78//AC005034
- F-HEMBA1002486
- 25 F-HEMBA1002495//HS\_3218\_B1\_A12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=23 Row=B, genomic survey sequence.//1.0:179:67//AQ181410
- 30 F-HEMBA1002498//Homo sapiens full-length insert cDNA clone ZD76B01.//1.4e-129:619:98//AF086404
- 35 F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.9e-24:306:68//AC004873
- F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799
- 40 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738:98//AJ011972
- 45 F-HEMBA1002515//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL022329
- 50 F-HEMBA1002538//HS\_2185\_B2\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339:78//AQ298315
- 55 F-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372:95//AQ188792

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- 5 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//3.5e-137:655:98//AF016903
- F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173:68//U31875
- 10 F-HEMBA1002555//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628:60//AC004670
- 15 F-HEMBA1002558//Human Xp22 BAC CT-285115 (from CalTech/Research Genetics) , PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366
- 20 F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538:66//AC003687
- F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//1.3e-140:457:99//AF075587
- 25 F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//5.1e-79:385:99//AQ038102
- 30 F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.9e-35:430:70//AC005940
- 35 F-HEMBA1002592//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4Ae-19:303:71//Z93403
- 40 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820:99//AB011169
- F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353:58//AC004413
- 45 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632:97//AB018351
- 50 F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792:58//AC004153
- F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:58//AL034446
- 55 F-HEMBA1002645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL031118

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F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859:99//AC004839

5 F-HEMBA1002659//Z.mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144:66//M32100

10 F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774:84//AC004535

F-HEMBA1002666

15 F-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL034421

20 F-HEMBA1002679//nbxb0002cC12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621

25 F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651:61//Z86099

F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306:81//AF060195

30 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327:62//AB007924

F-HEMBA1002712

35 F-HEMBA1002716//HS\_3064\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980

40 F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//6.1e-21:217:77//AC004782

45 F-HEMBA1002730//Human platelet glycoprotein IIIa (GPIIIa) gene, exon 1.//0.57:125:67//M57481

50 F-HEMBA1002742//RPCI11-39J10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102

55 F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//7.1e-70:303:82//AC003694

F-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//0.096:212:62//AL031732

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- 5 F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence.//6.7e-40:232:70//AC004622
- F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.0e-177:834:98//AB011126
- 10 F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.3e-140:840:88//E12829
- 15 F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic survey sequence.//1.1e-28:263:77//AL007965
- F-HEMBA1002779//CIT-HSP-23331.TF CIT-HSP Homo sapiens genomic clone 23331, genomic survey sequence.//1.8e-32:180:98//AQ036891
- 20 F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence.//7.0e-06:199:67//AC004592
- 25 F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu.//0.00015:244:67//X75756
- F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence.//0.0010:534:57//AL034558
- 30 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.1e-167:820:97//AF071185
- 35 F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-113:254:90//AC005043
- F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, complete cds.//1.2e-122:760:86//AF046870
- 40 F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235:65//AL022153
- 45 F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.4e-170:744:99//AC004707
- 50 F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//1.3e-05:334:59//AF069186
- 55 F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence.//2.9e-140:750:93//AQ028419
- F-HEMBA1002876//HS\_2270\_B1\_H03\_MF CIT Approved Human Genomic Sperm Library D

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Homo sapiens genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence.//0.44:163:64//AQ164031

5 F-HEMBA1002886

F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence.//0.00015:277:61//AC005195

10

F-HEMBA1002921

15 F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence.//0.0016:175:66//B89715

F-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797:98//AL031681

20

F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//4.9e-173:803:99//AB011148

25 F-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411:99//AL033531

30 F-HEMBA1002939//RPCI11-74O14.TJ RPCI11 Homo sapiens genomic clone R-74O14, genomic survey sequence.//1.7e-41:215:99//AQ266676

F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence.//1.7e-37:375:74//AQ082240

35

F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//0.00074:683:58//AC005578

40 F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence.//6.1e-24:250:78//AQ284146

45 F-HEMBA1002968//HS\_2262\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence.//0.99:270:60//AQ217059

50 F-HEMBA1002970//RPCI11-5L24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5L24, genomic survey sequence.//1.4e-10:189:71//B49289

F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence.//4.3e-21:181:80//AQ080538

55

F-HEMBA1002973//Rattus norvegicus Wistar 3',5'-cyclic AMP phosphodiesterase (PDE4-10) gene, exon 10.//2.5e-40:257:89//U01290



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- 5 F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797
- F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286
- 10 F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.5e-50:331:85//AC005484
- 15 F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//2.6e-20:357:66//AC005557
- 20 F-HEMBA1003034//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//4.5e-60:415:73//Z95704
- 25 F-HEMBA1003035//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//2.3e-05:591:57//AC004617
- F-HEMBA1003037//RPC111-88F2.TJ RPC111 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230:60//AQ286677
- 30 F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//8.1e-128:550:94//AC004983
- 35 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777:98//AF054182
- 40 F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//AC005505
- F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783
- 45 F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//1.5e-20:595:65//U72648
- 50 F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176:99//AQ080257
- 55 F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//9.4e-43:478:70//Z99297

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F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57:85//AC004673

5 F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548

10 F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734:58//AF001550

F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//113750

15 F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308

20 F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.00054:480:60//M58564

25 F-HEMBA1003129//HS\_3139\_B2\_F05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635

30 F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259

F-HEMBA1003136

35 F-HEMBA1003142//Homo sapiens full-length insert cDNA clone ZC39B06.//6.9e-121:563:100//AF086197

40 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:99//AJ005670

F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 @complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302

45 F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882

50 F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325

55 F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824

F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene,

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exon 1.//1.6e-05:367:61//U09302

- 5 F-HEMBA1003202//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//9.0e-23:247:73//AC004003
- 10 F-HEMBA1003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824
- F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.9e-31:158:86//AC002037
- 15 F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150
- 20 F-HEMBA1003222//RPC11-47P17.TJ RPC11 Homo sapiens genomic clone R-47P17, genomic survey sequence.//8.7e-39:202:99//AQ202885
- F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence.//0.86:227:62//AB019230
- 25 F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.6e-05:372:61//AE001373
- 30 F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=O, genomic survey sequence.//0.00032:57:96//B46142
- 35 F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein.//2.2e-08:531:59//X64624
- 40 F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII-fragment, SC6pA19H4.//0.070:267:64//Z78949
- F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 2301B4, genomic survey sequence.//5.2e-08:295:63//AQ015073
- 45 F-HEMBA1003278//HS\_3075\_A1\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence.//0.98:399:58//AQ120599
- 50 F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840
- 55 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds.//9.0e-145:539:97//AF038662

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F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5.0e-166:799:98//AB011109

5 F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551

10 F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//L17343

15 F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0.0017:210:64//AF051177

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//4.6e-188:865:99//AB001872

20 F-HEMBA1003322//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015

25 F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence.//8.4e-12:166:76//B67147

30 F-HEMBA1003328//HS\_2230\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313

35 F-HEMBA1003330//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555

40 F-HEMBA1003348//HS\_3194\_A1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779

F-HEMBA1003369//H.vulgare GAA-satellite DNA.//0.12:89:71//Z50100

45 F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence.//3.5e-32:199:80//AF024533

50 F-HEMBA1003373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405

F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U67229

55 F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSS, complete sequence.//4.6e-22:206:81//AL021528

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F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00094:72:90//AC006026

5 F-HEMBA1003395//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744

10 F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence.//2.4e-05:265:64//AQ056234

F-HEMBA1003403//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.3e-135:780:90//AC004066

15 F-HEMBA1003408

20 F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//1.9e-41:239:95//AL031321

F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3'UTR and trinucleotide repeat microsatellites.//2.2e-06:247:64//U08273

25 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds.//1.4e-149:697:99//AF051334

30 F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//1.7e-77:461:90//AC004066

35 F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, FliI (fliI) and FliJ (fliJ) genes, complete cds.//8.6e-08:752:58//U31090

F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//0.089:172:68//AC004098

40 F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//4.5e-150:562:97//AC005041

45 F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, complete cds.//4.7e-09:433:60//D16687

50 F-HEMBA1003531//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//2.3e-48:297:90//AC004990

F-HEMBA1003538//Human complement C1r mRNA, complete cds.//4.3e-22:474:63//M14058

55 F-HEMBA1003545//Rattus norvegicus (clone 1.6kB) islet-2 mRNA, complete cds.//3.5e-143:805:91//L35571

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F-HEMBA1003548

5 F-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
447E6, WORKING DRAFT SEQUENCE.//3.4e-58:331:83//AL031724

10 F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems  
Human BAC Library) complete sequence.//6.0e-99:703:84//AC005913

F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA,  
complete cds.//1.3e-99:587:89//J05071

15 F-HEMBA1003568//HS\_3149\_A1\_C04\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence.//4.1e-  
05:389:57//AQ166810

20 F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.6e-  
102:669:85//AC005539

25 F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds.//0.00033:  
649:58//U60170

30 F-HEMBA1003579//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
MAL1P1, WORKING DRAFT SEQUENCE.//0.00034:623:56//AL031744

F-HEMBA1003581//Mouse mRNA for talin.//3.3e-41:181:86//X56123

35 F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPCI-11\_192K18, complete  
sequence.//4.4e-70:273:94//AC006075

40 F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete  
sequence.//6.0e-17:768:58//AE001395

F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete  
sequence.//4.0e-09:777:56//AE001398

45 F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete  
sequence.//1.3e-146:692:98//AC005153

50 F-HEMBA1003615//HS\_2010\_A2\_A07\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence.//1.1e-  
22:137:97//AQ226592

55 F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//2.4e-169:501:  
97//AB015344

F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds.//4.7e-37:165:92//AF034080

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- 5 F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0024:514:58//AC005139
- F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence.//6.5e-15:358:63//B92984
- 10 F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-21:238:76//AC005077
- 15 F-HEMBA1003640//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING DRAFT SEQUENCE.//2.3e-15:371:63//Z85987
- F-HEMBA1003645//A.thaliana 81kb genomic sequence.//1.0:529:57//X98130
- 20 F-HEMBA1003646
- F-HEMBA1003656
- 25 F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.6e-175:824:98//AC005746
- 30 F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.1e-24:190:87//AC004765
- F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//AC005065
- 35 F-HEMBA1003680//H.sapiens DNA sequence.//7.3e-22:172:87//Z22322
- 40 F-HEMBA1003684//H.sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723
- F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691
- 45 F-HEMBA1003692
- F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//0.55:450:60//AC003101
- 50 F-HEMBA1003714
- 55 F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-16:316:68//AL023575

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F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:73//AC004056

5 F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey sequence.//1.1e-112:532:99//AQ079348

10 F-HEMBA1003729//HS\_3043\_A1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345

15 F-HEMBA1003733//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.7e-104:761:82//AC006213

20 F-HEMBA1003742//HS\_3027\_A2\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731

25 F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey sequence.//2.9e-10:310:63//AQ113513

F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194

30 F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139

35 F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496

F-HEMBA1003784//Caenorhabditis elegans cosmid C55B6.//0.054:463:58//U88181

40 F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGCR Region, complete sequence.//1.9e-44:425:76//AC000070

45 F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178

50 F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-138:275:99//AC004596

F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940

55 F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212



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- 5 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516
- F-HEMBA1003836//S.cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125
- 10 F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey sequence.//1.4e-45:180:90//B54810
- F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT9875K-1188B12 map 10p12.1, complete sequence.//0.0014:574:58//AC005875
- 15 F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300
- F-HEMBA1003866//Mus musculus semaphorin V1a mRNA, complete cds.//5.9e-81:853:71//AF030430
- 20 F-HEMBA1003879//H.sapiens CBP80 mRNA.//2.0e-08:87:95//X80030
- 25 F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036
- F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//AC004079
- 30 F-HEMBA1003893//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b6, forward read cpg11b6.ft1a.//3.6e-32:173:99//Z59012
- 35 F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26M20, genomic survey sequence.//8.2e-12:422:61//AQ003455
- 40 F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:468:58//AE001401
- F-HEMBA1003926//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING DRAFT SEQUENCE.//3.6e-27:278:76//AL031658
- 45 F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:315:81//AF109718
- 50 F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequence.//6.1e-09:413:63//B38195
- 55 F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65//AC005140

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F-HEMBA1003950//M.capricolum DNA for CONTIG MC072.//0.029:458:58//Z33058

5 F-HEMBA1003953//HS\_2268\_A1\_B04\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey sequence.//9.0e-  
07:239:64//AQ085098

10 F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete  
sequence.//2.8e-57:424:74//AC004894

F-HEMBA1003959//RPC111-78E8.TV RPC111 Homo sapiens genomic clone R-78E8,  
15 genomic survey sequence.//4.3e-86:441:9611AQ285498

F-HEMBA1003976//HS\_3146\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3146 Col=17 Row=O, genomic survey sequence.//6.3e-  
20 10:129:80//AQ141146

F-HEMBA1003978

25 F-HEMBA1003985//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
clone Y105C5, WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855

F-HEMBA1003987

30

F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9.//0.40:238:61//AL034446

F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2.//2.0e-07:116:70//U19354  
35

F-HEMBA1004011//Plasmodium falciparum 3D7, chromosome 12 PFYAC588 genomic  
sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.098:286:60//AC004710

40 F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete  
sequence.//2.8e-185:896:97//AC005670

F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete  
45 sequence.//6.3e-68:417:80//AC005411

F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human  
BAC Library) complete sequence.//2.0e-47:418:77//AC005859  
50

F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28,  
WORKING DRAFT SEQUENCE.//1.6e-51:564:74//AP000052

55 F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete  
sequence.//1.2e-05:636:55//AE001398

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F-HEMBA1004045//Homo sapiens (subclone 1\_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:373:76//AC002252

5 F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039:234:63//D63393

10 F-HEMBA1004049//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//4.8e-135:780:89//AC003106

F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:457:58//L13435

15 F-HEMBA1004056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//3.3e-25:246:77//AL021977

20 F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey sequence.//7.8e-24:233:76//B68555

25 F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08:614:59//U49822

30 F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//AF091234

35 F-HEMBA1004111//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160

F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence.//8.7e-24:320:71//AF046393

40 F-HEMBA1004132//HS\_3226\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017

45 F-HEMBA1004133

50 F-HEMBA1004138//HS\_3036\_B1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=N, genomic survey sequence.//0.0035:165:64//AQ294763

F-HEMBA1004143

55 F-HEMBA1004146

F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains

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CA repeats, STS.//0.00011:618:60//Z96811

5 F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913

10 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855

F-HEMBA1004199

15 F-HEMBA1004200//HS\_2015\_A1\_B05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957

20 F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268\_P\_23, complete sequence.//7.8e-59:216:83//AC004807

25 F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488

F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748

30 F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424

35 F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927

F-HEMBA1004238

40 F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708

45 F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010

50 F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6). mRNA, complete cds.//1.7e-30:315 :74//L13619

55 F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693

F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//3.1e-78:335:87//AC004707

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- 5 F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831
- F-HEMBA1004274//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-  
28:153:100//AQ136993
- 10 F-HEMBA1004275//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051
- 15 F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6,  
genomic survey sequence.//5.0e-07:63:98//AQ240477
- 20 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete  
cds.//2.1e-185:868:99//AF022795
- F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23,  
complete sequence.//1.0:387:59//AB013395
- 25 F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-  
06:92:89//AB012254
- 30 F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:  
59//AC004897
- 35 F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment  
2/4.//0.28:522:57//AJ235271
- F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete  
sequence.//7.1e-136:548:92//AC006130
- 40 F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:  
320:65//Z84720
- 45 F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:  
62//AB011094
- 50 F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//7.0e-168:895:93//AC004995
- F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library)  
complete sequence.//4.6e-73:713:75//AC002980
- 55 F-HEMBA1004335//Human DNA-sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498

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F-HEMBA1004341

5 F-HEMBA1004353//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571

10 F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.1e-45:190:92//U75968

F-HEMBA1004356

15 F-HEMBA1004366//P.falciparum complete gene map of plastid-like DNA (IR-A).//2.2e-07:736:57//X95275

20 F-HEMBA1004372//H.sapiens dystrophin gene intron 44.//1.0:129:62//X77644

F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//4.7e-42:237:94//M21977

25 F-HEMBA1004394//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//5.2e-05:519:59//AE001402

30 F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence.//4.0e-32:261:76//AC002463

35 F-HEMBA1004405//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.4e-07:693:58//AC005507

F-HEMBA1004408//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-69:195:100//AC005037

40 F-HEMBA1004429//HS\_3193\_A1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3193 Col=11 Row=C, genomic survey sequence.//5.1e-67:386:91//AQ172942

45 F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//3.2e-27:242:82//AC002554

50 F-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.7e-75:590:81//AC004846

55 F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, complete sequence.//0.045:215:66//AL034407

F-HEMBA1004479//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//5.2e-43:364:79//AF060194

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- 5 F-HEMBA1004482//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//6.8e-17:791:59//AC005505
- F-HEMBA1004499//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//4.4e-125:251:94//AC004686
- 10 F-HEMBA1004502//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.012:635:57//AC004709
- F-HEMBA1004506//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.8e-127:766:88//AC004453
- 15 F-HEMBA1004507
- 20 F-HEMBA1004509//Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAI project).//1.0e-13:244:67//AL021712
- F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280).//1.6e-72:678:74//X53416
- 25 F-HEMBA1004538//Sequence 1 from patent US 5612190.//0.00015:416:59//I36871
- 30 F-HEMBA1004542//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.95:202:64//AC005038
- F-HEMBA1004554//Arabidopsis thaliana BAC T26D22.//0.45:624:56//AFO58826
- 35 F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//9.1e-10:173:70//D87457
- 40 F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence.//6.1e-23:134:73//AC002542
- F-HEMBA1004577//Homo sapiens Chromosome 16 BAC clone CIT987SK-582J2, complete sequence.//1.6e-15:190:77//AC004525
- 45 F-HEMBA1004586//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-31:388:76//AC004895
- 50 F-HEMBA1004596//RPCI11-81O21.TJ RPCI11 Homo sapiens genomic clone R-81O21, genomic survey sequence.//2.2e-90:458:90//AQ285136
- 55 F-HEMBA1004604//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//8.6e-105:699:84//AF071316

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F-HEMBA1004610//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//5.4e-20:267:72//AC004983

5 F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP Homo sapiens genomic clone 2319H15, genomic survey sequence.//6.2e-26:147:99//AQ034944

10 F-HEMBA1004629//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.6e-06:766:56//AC005504

15 F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//4.7e-73:412:92//Z83843

20 F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EHV1 ORF 46, VZV ORF 44.//0.92:181:61//X90418

F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//7.8e-47:784:65//X74904

25 F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds.//6.4e-06:458:61//AF004431

30 F-HEMBA1004666//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.30:733:55//Z98865

35 F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//7.5e-136:521:98//AL031432

40 F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence.//0.43:365 :59//AC000045

F-HEMBA1004672

45 F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.096:651:54//AC005308

50 F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey sequence.//0.23:238:65//AQ040642

55 F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC11-93D11 (from Roswell Park Cancer Center) complete sequence.//2.1e-27:375:72//AC002357

F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.6e-36:191:91//AC006210



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- 5 F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.1e-133:639:99//AC005562
- F-HEMBA1004725//RPCI11-75013.TJ RPCI11 Homo sapiens genomic clone R-75O13, genomic survey sequence.//6.2e-32:169:100//AQ266512
- 10 F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence.//8.0e-68:732:72//AC004029
- 15 F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey sequence.//4.9e-18:209:69//AQ017556
- 20 F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//1.8e-13:451:62//AF028340
- 25 F-HEMBA1004736//Human DNA Sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//5.0e-87:646:78//Z94056
- 30 F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence.//0.24:526:57//AC002461
- F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-25:268:76//AC004913
- 35 F-HEMBA1004752//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//1.1e-07:503:61//X83546
- 40 F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence.//4.5e-38:314:81//AC000028
- F-HEMBA1004756//Homo sapiens, complete sequence.//1.4e-111:326:84//AC005854
- 45 F-HEMBA1004758//Sequence 29 from patent US 5534410.//3.9e-135:769:91//23472
- 50 F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds.//3.6e-47:404:79//U75285
- F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.//6.7e-107:890:78//AC004941
- 55 F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-09:806:59//AC004709

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F-HEMBA1004771//G.muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA.//0.69:239:61//X65063

5 F-HEMBA1004776

F-HEMBA1004778

10 F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds.//3.4e-46:778:64//AF003622

15 F-HEMBA1004803//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.3e-82:580:82//AC004617

20 F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//5.4e-07:642:59//AC005083

F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3.//1.4e-46:171:92//L01042

25 F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14.//3.5e-31:546:66//M86257

30 F-HEMBA1004820//C.botulinum progenitor toxin complex genes.//0.0014:343:62//X87972

F-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//1.5e-85:512:88//X53744

35 F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFB1) gene, exon 1.//0.0065:284:61//AF054590

40 F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence.//0.92:250:59//AC000400

F-HEMBA1004864

45 F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//3.6e-12:214:72//AL031120

50 F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.1e-08:255:69//AC004020

55 F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.062:155:69//U32943

F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence.//0.00055:323:60//L12043

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- 5 F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence.//9.6e-16:166:80//AC003051
- F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial.//0.81:146:65//M94003
- 10 F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmid R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//1.4e-36:338:78//AC003006
- 15 F-HEMBA1004929//CIT-HSP-2373116.TR CIT-HSP Homo sapiens genomic clone 2373116, genomic survey sequence.//2.4e-86:443:96//AQ108676
- 20 F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence.//4.6e-20:219:73//AC004109
- F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence.//1.4e-28:216:85//B30726
- 25 F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence.//0.53:222:61//AF042091
- 30 F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-58:509:78//AC005482
- 35 F-HEMBA1004954//HS\_2033\_A2\_A08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence.//3.7e-47:243:99//AQ229758
- 40 F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.048:421:58//X95276
- 45 F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8.//0.89:333:58//Z97343
- F-HEMBA1004972
- 50 F-HEMBA1004973//RPCI11-66P8.TK RPCI11 Homo sapiens genomic clone R-66P8, genomic survey sequence.//3.5e-22:245:77//AQ238471
- 55 F-HEMBA1004977//Homo sapiens full-length insert cDNA clone YZ83B08.//9.0e-11:84:98//AF086080
- F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10,

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genomic survey sequence.//0.0021:152:66//AQ075713

- 5 F-HEMBA1004980//HS\_3018\_A2\_E04\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey sequence.//1.9e-77:  
392:97//AQ071873
- 10 F-HEMBA1004983//Albinaria corrugata isolate cor. Prn1.1 16S ribosomal RNA gene,  
mitochondrial gene for mitochondrial RNA, partial sequence.//0.0030:276:61//AF031680
- 15 F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (LANL),  
complete sequence.//4.2e-138:640:99//AC005590
- 20 F-HEMBA1005008//Human mariner1 transposase gene, complete consensus  
sequence.//6.8e-20:160:88//U52077
- 25 F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//2.0e-144:668:  
99//AF041474
- 30 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//1.4e-146:693:  
98//AB014548
- 35 F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome  
6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE  
pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c),  
H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs,  
GSSs and genomic marker D6S464, complete sequence.//2.2e-115:668:90//AL009179
- 40 F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete  
sequence.//4.6e-138:591:98//AC004596
- 45 F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5,  
genomic survey sequence.//3.7e-61:271:88//AQ055486
- 50 F-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//3.8e-17:218:73//Z22819
- 55 F-HEMBA1005050//Human Tis11d gene, complete cds.//0.079:251:63//U07802
- F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic  
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.018:560:56//AC004688
- F-HEMBA1005066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
774G10, WORKING DRAFT SEQUENCE.//3.4e-97:432:84//AL034410
- F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//6.9e-  
07:176:68//X76589

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F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence.//2.1e-48:274:93//AQ038720

5 F-HEMBA1005083//HS\_2248\_B1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence.//3.4e-06:230:64//AQ129575

10 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//1.3e-161:762:98//AF080561

15 F-HEMBA1005113//L.esculentum microsatellite repeat DNA region.//0.0038:742:57//X90770

F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.6e-83:479:78//AC004854

20 F-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//3.9e-24:576:64//AL023808

25 F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//4.7e-36:283:80//AC004542

30 F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//5.0e-10:332:64//AC004469

F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//4.0e-10:734:58//AP000023

35 F-HEMBA1005185//H.sapiens CpG island DNA genomic Mse1 fragment, clone 91b2, forward read cpg91b2.ft1a.//12.2e-14:93:100//Z63847

40 F-HEMBA1005201//Drosophila melanogaster cosmid 152A3.//4.7e-35:679:64//AL009194

F-HEMBA1005202//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.7e-138:778:90//X53744

45 F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene.//7.1e-12:376:62//AJ011320

50 F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds.//7.1e-05:411:60//AB007914

55 F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.5e-06:212:66//AC004542

F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-07:625:57//AC005308

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- 5 F-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//8.7e-45:567:72//AC005154
- F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.//0.96:298:62//AC002365
- 10 F-HEMBA1005251
- F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.5e-160:392:99//AC005837
- 15 F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.3e-05:496:60//AF069291
- 20 F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//5.7e-05:220:64//AL033521
- 25 F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//2.4e-20:338:65//U97018
- F-HEMBA1005296
- 30 F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//1.6e-51:381:78//AL031012
- F-HEMBA1005311
- 35 F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//0.94:226:63//AP000031
- 40 F-HEMBA1005315//Homo sapiens BAC810, complete sequence.//9.5e-15:684:62//U85198
- F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone.//2.6e-05:472:59//Z83823
- 45 F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//3.3e-90:300:90//AC005803
- 50 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//1.4e-151:740:97//AJ007581
- F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence.//2.1e-86:438:97//AQ016145
- 55 F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds.//1.8e-98:500:88//U09414

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- 5 F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds.//8.3e-72:577:73//AF047714
- F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS.//1.3e-07:274:66//Z82900
- 10 F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.9e-48:611:69//AC004813
- 15 F-HEMBA1005382//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//1.6e-27:154:98//AQ103204
- 20 F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence.//4.0e-07:443:61//M23175
- 25 F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey sequence.//7.6e-17:225:71//AQ076749
- F-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//4.5e-131:278:98//AL034379
- 30 F-HEMBA1005408//HS\_3007\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence.//8.0e-06:218:66//AQ294366
- 35 F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS.//1.5e-41:432:76//Z73496
- 40 F-HEMBA1005411
- F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//1.0e-169:537:99//AF041248
- 45 F-HEMBA1005426
- F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-37:260:76//AC006130
- 50 F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence.//5.0e-133:631:98//B93234
- 55 F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.5e-118:868:83//AL022576

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- 5 F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//1.2e-179:838:99//AC005212
- F-HEMBA1005472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//3.4e-20:187:74//AL031985
- 10 F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//4.1e-22:445:65//AP000041
- F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey sequence.//6.7e-51:269:97//AQ026941
- 15 F-HEMBA1005497//HS\_3097\_A2\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic survey sequence.//1.4e-66:345:96//AQ103810
- F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//5.4e-178:818:98//AC004957
- 25 F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:98//L12147
- 30 F-HEMBA1005508//Homo sapiens clone hRPK.1\_A\_1, complete sequence.//0.00012:455:60//AC006196
- F-HEMBA1005511//Homo sapiens MHC class 1 region.//3.3e-43:421:77//AF055066
- 35 F-HEMBA1005513//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//2.3e-20:352:69//U71219
- 40 F-HEMBA1005517//Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate E7.//2.5e-08:431:62//AJ001216
- F-HEMBA1005518//M.musculus mRNA for paladin gene.//8.2e-90:651:81//X99384
- 45 F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.8e-167:755:99//AC004913
- 50 F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//2.4e-42:475:73//AC006241
- 55 F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds.//1.2e-94:512:92//U21855
- F-HEMBA1005530



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- 5 F-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING DRAFT SEQUENCE.//9.4e-87:422:99//AL034431
- F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743
- 10 F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377
- F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153
- 15 F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407
- 20 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932
- 25 F-HEMBA1005577//HS-1004-A1-E11 -MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971
- 30 F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531
- F-HEMBA1005582//HS\_3242\_A1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275
- 35 F-HEMBA1005583
- 40 F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025
- 45 F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.3e-158:748:99//AC005746
- 50 F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527
- F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP Homo sapiens genomic clone 2326I6, genomic survey sequence.//0.0014:132:70//AQ041484
- 55 F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089

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- 5 F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome Xq21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175
- 10 F-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731
- F-HEMBA1005627//RPCI11-34P9 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110
- 15 F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460
- 20 F-HEMBA1005632
- F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036
- 25 F-HEMBA1005666
- F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//AC004850
- 30 F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478
- 35 F-HEMBA1005680
- F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742
- 40 F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001
- 45 F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513
- 50 F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348
- F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697
- 55 F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//AC005156

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- 5 F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8,  
genomic survey sequence.//1.3e-18:113:100//AQ238535
- 10 F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome  
Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms,  
complete sequence.//3.6e-56:764:70//Z97181
- 15 F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter  
contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196
- 20 F-HEMBA1005780//RPCI11-74E19.TJ RPCI11 Homo sapiens genomic clone R-74E19,  
genomic survey sequence.//0.0011:283:62//AQ268432
- 25 F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete  
sequence.//0.14:326:61//AC004079
- F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:  
59//X92523
- 30 F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered  
pieces.//0.87:417:56//AC003020
- F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR  
Region, complete sequence.//8.8e-42:370:79//AC000094
- 35 F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2.  
Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated,  
actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S  
Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete  
sequence.//2.1e-42:690:67//AL022577
- 40 F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey  
sequence.//4.3e-07:253:59//AL018749
- 45 F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone-2289L23,  
genomic survey sequence.//2.2e-68:333:99//B98952
- 50 F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete  
sequence.//1.9e-57:331:87//AC005351
- 55 F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete  
sequence.//5.1e-182:864:98//AC004945
- F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered  
pieces.//3.0e-44:340:80//AC004086

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- 5 F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026
- 10 F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584
- 15 F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.3e-41:431:77//AC005666
- 20 F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPCI4-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086
- 25 F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974
- 30 F-HEMBA1005962//RPCI11-17O15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821
- 35 F-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//9.3e-73:372:97//AQ147357
- 40 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516
- 45 F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408
- 50 F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599
- 55 F-HEMBA1006002
- F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405
- F-HEMBA1006031
- F-HEMBA1006035
- F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:

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74//D87009

- 5 F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:7011AC005386
- 10 F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153
- F-HEMBA1006081
- 15 F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500
- F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098
- 20 F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880
- 25 F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte-Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177
- 30 F-HEMBA1006121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672
- 35 F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966
- 40 F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085
- 45 F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162
- 50 F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500
- F-HEMBA1006155//H.sapiens CpG island DNA genomic Mse1 fragment, clone 119b6, forward read cpg119b6.ft1a.//1.0:85:72//Z64428
- 55 F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693

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F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt]//8.4e-50:642:73//S49400

5 F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22:194:74//AC005318

10 F-HEMBA1006198

F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557

15 F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074

20 F-HEMBA1006252//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664

F-HEMBA1006253

25 F-HEMBA1006259//HS\_2231\_A1\_D10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722

30 F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673

35 F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791

F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134

40 F-HEMBA1006283

45 F-HEMBA1006284//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289

50 F-HEMBA1006291//HS\_2208\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804

F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415

55 F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070

F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183

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- 5 F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074
- 10 F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563
- 15 F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420
- 20 F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//1.6e-31:484:68//U71219
- 25 F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671
- 30 F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244
- 35 F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413
- 40 F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence.//3.0e-57:401:81//AC002327
- 45 F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence.//1.3e-110:525:99//B92570
- 50 F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence.//4.4e-05:163:70//B37813
- 55 F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC004806
- F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//3.7e-15:157:78//AC005179
- F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//1.2e-39:752:63//AL022165

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- 5 F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//2.4e-41:438:76//AF107885
- 10 F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//0.027:293:64//AL031781
- 15 F-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930
- 20 F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.051:440:59//X04465
- F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds.//1.0:238:59//U62088
- 25 F-HEMBA1006446//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749
- 30 F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560
- F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.0:293:59//AC006120
- 35 F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709
- 40 F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247
- 45 F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence.//2.9e-48:286:84//AC004752
- F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.96:283:59//AC006031
- 50 F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577
- 55 F-HEMBA1006489//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone



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467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283

5 F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//6.0e-122:337:100//AC005828

10 F-HEMBA1006494//Homo sapiens chromosome 7qtelo BAC E3, complete sequence.//3.8e-23:459:68//AF093117

F-HEMBA1006497//HS\_3023\_B2\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence.//2.3e-81:433:95//AQ093846

15 F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19b).//1.6e-13:86:87//X62364

20 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//2.3e-139:470:98//AB014566

25 F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence.//4.3e-27:406:71//AC003991

F-HEMBA1006530//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//2.9e-27:408:65//AL031650

30 F-HEMBA1006535//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.028:599:60//AL034557

35 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.//1.4e-171:654:98//AF093419

40 F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//3.8e-104:811:80//Z73986

45 F-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//4.8e-99:386:82//U06944

F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1.//0.012:322:60//U21925

50 F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0026:580:58//AC005504

55 F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//6.3e-08:231:70//U39357

F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence.//0.036:250:62//AQ197107

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- 5 F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.0:225:63//AL021841
- F-HEMBA1006595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156
- 10 F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166
- 15 F-HEMBA1006612//RPCI11-88F20.TJ RPCI11 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726
- 20 F-HEMBA1006617//HS\_2193\_B2\_H07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685
- 25 F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284
- 30 F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//9.6e-112:800:83//AC002036
- 35 F-HEMBA1006635//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745
- 40 F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP) mRNA, complete cds.//9.6e-15:318:68//AF032896
- F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.58:254:65//AC006148
- 45 F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds.//1.5e-37:108:88//U94479
- 50 F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//1.3e-154:671:96//AC005601
- F-HEMBA1006653
- 55 F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//5.2e-110:254:93//AC005189

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F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//1.4e-14:177:76//AC004554

5 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15:122:90//Y12065

10 F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//0.098:218:63//AC004755

15 F-HEMBA1006682//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346

F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-22:151:78//AC006011

20 F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738

F-HEMBA1006708

25 F-HEMBA1006709

30 F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.3e-08:136:79//AC005537

35 F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//5.8e-162:497:98//AC005828

F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796

40 F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.//4.1e-129:804:85//Z83850

45 F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//2.2e-162:766:99//AC005752

50 F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465

55 F-HEMBA1006779//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//1.4e-103:355:87//AL022727

F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7,

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genomic survey sequence.//0.072:147:68//AQ077208

5 F-HEMBA1006789//nbxb0037113r CUGI Rice BAC Library Oryza sativa genomic clone  
nbxb0037113r, genomic survey sequence.//0.00011:288:63//AQ290474

10 F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3,  
genomic survey sequence.//5.1e-80:420:96//AQ020511

F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U79298

15 F-HEMBA1006807//Homo sapiens mRNA for SPOP.//1.2e-66:651:73//AJ000644

F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete  
sequence.//6.0e-116:541:99//AC004797

20 F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete  
sequence.//0.40:159:66//AC004262

25 F-HEMBA1006832//Homo sapiens (subclone 3\_g8 from P1 H25) DNA sequence, complete  
sequence.//1.8e-24:323:71//AC002196

30 F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium  
cancer, segment 4/10.//0.15:403:60//AB020872

F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete  
sequence.//0.20:472:57//AE001369

35 F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.4e-79:641:  
76//AF046757

40 F-HEMBA1006885//HS\_2208\_B2\_G06\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence.//4.9e-  
18:206:76//AQ089246

45 F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3  
Contains EST, GSS, complete sequence.//5.4e-07:298:65//AL031321

F-HEMBA1006914//S.pombe chromosome II cosmid c16H5.//0.00040:194:66//AL022104

50 F-HEMBA1006921//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete  
sequence.//1.1e-174:813:99//AC006027

55 F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF036704

F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A).//4.0e-06:739:  
57//X95275

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F-HEMBA1006936

5 F-HEMBA1006938//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
MAL1P4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747

10 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-90:437:  
98//AJ010841

15 F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. contains  
STS and polymorphic CA repeat.//0.67:217:62//Z82205

F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6e-  
143:740:94//AF004828

20 F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:338:89//E06058

F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete  
sequence.//7.1e-31:536:66//AC003071

25 F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT  
SEQUENCE.//9.5e-07:285:60//Z82209

30 F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete  
sequence.//0.99:388:58//AC002328

35 F-HEMBA1007017//Sequence 3 from Patent WO9416067.//0.96:220:62//A39358

F-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//1.3e-124:838:83//X79088

40 F-HEMBA1007045

F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.17:  
343:60//Z99281

45 F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.3e-67:  
659:74//U85056

50 F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572

F-HEMBA1007066//HS\_3116\_A2\_A03\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:  
214:62//AQ140467

55 F-HEMBA1007073//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer  
Institute Human PAC library) complete sequence.//9.3e-54:519:68//AC004242

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- 5 F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6,  
genomic survey sequence.//8.7e-80:387:98//AQ044076
- F-HEMBA1007080
- 10 F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1.//3.5e-06:496:59//AL034447
- F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence.//7.4e-07:553:  
56//Z98551
- 15 F-HEMBA1007112//HS\_2171\_A1\_B01\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence.//1.0:  
172:61//AQ091865
- 20 F-HEMBA1007113//Human DNA sequence from clone 1044O17 on chromosome Xp11.3-  
11.4 Contains GSS and STS, complete sequence.//0.54:502:56//AL023875
- F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430.//1.4e-08:265:64//U42833
- 25 F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5,  
genomic survey sequence.//0.97:267:62//AQ264035
- 30 F-HEMBA1007147//HS\_3208\_A2\_C04\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence.//9.1e-  
90:466:95//AQ176696
- 35 F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete  
sequence.//6.0e-138:524:98//AC005239
- F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6,  
40 genomic survey sequence.//2.0e-20:157:87//AQ280780
- F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds.//2.0e-62:318:  
45 97//AF062085
- F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING  
DRAFT SEQUENCE, 129 ordered pieces.//1.6e-21:205:80//AC005911
- 50 F-HEMBA1007194//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.3e-  
11:87:96//AQ187492
- 55 F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.7e-156:478:  
98//D86987

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- F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.024:342:63//AC004223
- 5 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//5.0e-176:839:98//AB018340
- 10 F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//4.3e-58:687:68//J00060
- F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//0.084:177:62//V00899
- 15 F-HEMBA1007256//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//1.3e-75:490:88//AL022240
- 20 F-HEMBA1007267//HS\_3218\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence.//2.9e-62:393:87//AQ181128
- 25 F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//1.1e-63:314:99//B95401
- 30 F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//3.1e-31:401:72//AC004638
- 35 F-HEMBA1007281//HS\_3115\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence.//5.0e-70:372:96//AQ186691
- 40 F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//1.2e-152:727:98//AL031003
- 45 F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphodiesterase, complete cds.//2.1e-21:542:63//AB008467
- 50 F-HEMBA1007301//COL1A1=type I collagen pro alpha 1(I) chain propeptide {3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 855 nt].//1.7e-08:388:61//S64596
- 55 F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence.//6.0e-84:390:75//AC000399
- F-HEMBA1007320
- F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence.//0.091:260:64//AC004485

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F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.12:472:59//AC005140

5 F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.5e-18:408:64//AC006120

10 F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//8.7e-25:500:62//AC005377

15 F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete sequence.//0.75:269:61//AC005738

F-HEMBB1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//5.0e-05:441:60//AC004617

20 F-HEMBB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491

25 F-HEMBB1000018//HS\_2179\_B2\_E04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250

30 F-HEMBB1000024//Human DNA sequence from PAC 106i20 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369

35 F-HEMBB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938

F-HEMBB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173

40 F-HEMBB1000036//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857

45 F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928

50 F-HEMBB1000039//HS\_2167\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404

55 F-HEMBB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164

F-HEMBB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507



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- 5 F-HEMBB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170
- 10 F-HEMBB1000054//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349
- 15 F-HEMBB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880
- 20 F-HEMBB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096
- F-HEMBB1000083
- 25 F-HEMBB1000089//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744
- 30 F-HEMBB1000099//Homo sapiens chromosome 18 BAC RPC11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909
- 35 F-HEMBB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210
- F-HEMBB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450
- 40 F-HEMBB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521
- 45 F-HEMBB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697
- F-HEMBB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090
- 50 F-HEMBB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542
- 55 F-HEMBB1000173//Homo sapiens 12q24 BAC RPC11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//9.4e-160:562:93//AC002996
- F-HEMBB1000175

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- 5 F-HEMBB1000198//HS\_3071\_A2\_A10\_MF CIT, Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388
- 10 F-HEMBB1000215//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence.//6.7e-17:138:86//AC005839
- 15 F-HEMBB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808
- 20 F-HEMBB1000218//Caenorhabditis elegans cosmid C52A11, complete sequence.//0.90:337:56//Z46792
- 25 F-HEMBB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.7e-90:175:92//Z69890
- 30 F-HEMBB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence.//0.16:171:62//U07918
- 35 F-HEMBB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.8e-08:355:63//AC005522
- 40 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds.//6.6e-155:735:98//AF075587
- 45 F-HEMBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16.//0.58:396:59//M98818
- 50 F-HEMBB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.4e-32:100:100//U75968
- 55 F-HEMBB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.8e-16:176:78//AC004470
- 60 F-HEMBB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.011:379:58//AE001369
- 65 F-HEMBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAI project).//0.92:272:61//AL022580
- 70 F-HEMBB1000284//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//0.00071:568:57//AC002366

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F-HEM BB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene.//3.0e-13:439:65//Z98745

5

F-HEM BB1000312//Homo sapiens clone GS051M12, complete sequence.//0.031:252:65//AC005007

10

F-HEM BB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence.//0.00033:173:65//AL026242

15

F-HEM BB1000318//HS\_3244\_B2\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence.//3.9e-85:438:95//AQ252951

20

F-HEM BB1000335//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//0.63:285:61//AC005968

F-HEM BB1000336

25

F-HEM BB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence.//0.0014:309:64//AC004051

30

F-HEM BB1000338//HS\_3108\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence.//3.8e-09:331:63//AQ140356

35

F-HEM BB1000339//Homo sapiens 12q24 PAC RPCI1-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-52:295:77//AC002351

F-HEM BB1000341

40

F-HEM BB1000343//Plasmodium falciparum MAL3P3, complete sequence.//0.00081:397:61//Z98547

45

F-HEM BB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//9.1e-34:596:66//AL020989

50

F-HEM BB1000369//Genomic sequence from Human 17, complete sequence.//0.012:298:60//AC002090

55

F-HEM BB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//9.3e-69:294:89//U96409

F-HEM BB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//3.5e-54:352:

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88//AL034377

- 5 F-HEM BB1000391//*Trichothecium roseum* internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.//0.011:168:67//U51982
- 10 F-HEM BB1000399//*Homo sapiens* Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98//AF076838
- 15 F-HEM BB1000402//*Homo sapiens* Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.7e-15:466:63//AC002368
- 20 F-HEM BB1000404//*Homo sapiens* mRNA for myosin-IXA.//3.5e-65:324:98//AJ001714
- 25 F-HEM BB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1 through D11S25, complete sequence.//0.013:399:62//AC001228
- 30 F-HEM BB1000434//*Homo sapiens* PAC clone 278C19 from 12q, complete sequence.//6.1e-83:571:84//AC004263
- 35 F-HEM BB1000438//RPCI11-21E14.TP RPCI-11 *Homo sapiens* genomic clone RPCI-11-21E14, genomic survey sequence.//0.0030:295:63//B83110
- 40 F-HEM BB1000441//*Homo sapiens* Chromosome 22q12 Cosmid Clone ll47g11, complete sequence.//2.5e-33:372:72//AC000035
- 45 F-HEM BB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821
- 50 F-HEM BB1000455//*Saccharomyces cerevisiae* mitochondrion origin of replication (ori6) and oli1 gene, complete cds.//0.016:522:58//L36899
- F-HEM BB1000472
- 55 F-HEM BB1000480
- F-HEM BB1000487//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING DRAFT SEQUENCE.//0.00013:314:64//Z98742
- 50 F-HEM BB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//4.1e-110:529:98//AL034423
- 55 F-HEM BB1000491//*Plasmodium falciparum* chromosome 2, section 25 of 73 of the complete sequence.//0.10:187:65//AE001388

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- 5 F-HEM BB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-06:637:58//AL022577
- 10 F-HEM BB1000510//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//3.1e-96:737:81//AC005553
- 15 F-HEM BB1000518//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.00014:163:68//AC004676
- F-HEM BB1000523//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.41:349:56//AL010212
- 20 F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:96//Y11710
- 25 F-HEM BB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//3.9e-56:683:71//AB020860
- 30 F-HEM BB1000554//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//2.2e-51:282:84//AJ011929
- 35 F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds.//6.1e-32:537:65//AB018293
- F-HEM BB1000564
- 40 F-HEM BB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-33:268:73//AC005077
- 45 F-HEM BB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//5.8e-47:734:66//AL022476
- 50 F-HEM BB1000586//H.sapiens highly polymorphic microsatellite DNA.//0.030:147:67//X79883
- F-HEM BB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.3e-41:278:83//AC002300
- 55 F-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.1e-182:871:98//AC005184

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- 5 F-HEM BB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19.//0.012:185:64//AF009074
- F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence.//1.2e-131:353:93//AF053356
- 10 F-HEM BB1000598//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.1e-58:600:72//AC006207
- F-HEM BB1000623//cDNA encoding Coliolum manganese peroxidase.//0.89:284:62//E12284
- 15 F-HEM BB1000630//Mus musculus clone NSAT47 nonsatellite RNA sequence.//1.9e-15:129:87//U26231
- 20 F-HEM BB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//80057
- F-HEM BB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811:65//AB002349
- 25 F-HEM BB1000637//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.1e-58:649:73//AC005478
- 30 F-HEM BB1000638//HS\_3051\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence.//0.0032:497:56//AQ155234
- 35 F-HEM BB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:791:68//AC005077
- F-HEM BB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//5.2e-64:775:69//AC003009
- 40 F-HEM BB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.7e-52:334:89//AC006186
- 45 F-HEM BB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//0.0062:426:60//AL024493
- 50 F-HEM BB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//9.6e-95:399:78//Z84488
- 55 F-HEM BB1000673//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//3.8e-

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50:293:92//AQ155121

5 F-HEMBB1000684//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE.//8.0e-65:282:83//Z93241

10 F-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds.//1.6e-118:575:97//AF040723

15 F-HEMBB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.6e-07:251:61//AC005507

20 F-HEMBB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//2.9e-20:434:64//AL031118

25 F-HEMBB1000709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//0.26:184:65//AL034554

30 F-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//1.8e-129:692:93//U53475

35 F-HEMBB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.7e-40:304:80//U91321

40 F-HEMBB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//8.9e-35:582:63//AF011889

45 F-HEMBB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//6.2e-46:262:89//AC005849

50 F-HEMBB1000763//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.6e-99:316:98//AL034405

55 F-HEMBB1000770//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//0.044:325:60//AL022727

F-HEMBB1000774

50 F-HEMBB1000781//Sequence 3 from patent US 5753446.//1.2e-92:599:86//AR008277

55 F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds.//9.3e-64:672:71//AB014577

F-HEMBB1000790//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.4e-41:460:74//AC004801

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- 5 F-HEMBB1000794//HS\_3034\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence.//1.8e-  
74:378:97//AQ117099
- 10 F-HEMBB1000807//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39d7, reverse  
read cpg39d7.rt1a.//8.5e-14:95:97//Z58412
- F-HEMBB1000810//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment,  
clone 303a8, complete read.//3.2e-05:138:71//Z79983
- 15 F-HEMBB1000821//HS\_2168\_B1\_A12\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey  
sequence.//0.85 :208:60//AQ086361
- 20 F-HEMBB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence.//3.0e-  
06:361:60//AC003015
- 25 F-HEMBB1000826//Human BAC clone RG180F08 from 7q31, complete sequence.//1.1e-27:  
360:69//AC002431
- F-HEMBB1000827
- 30 F-HEMBB1000831
- F-HEMBB1000835//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3.  
Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//0.00098:  
35 234:63//AL023581
- F-HEMBB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence.//4.5e-  
61:328:79//U73649
- 40 F-HEMBB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24.  
Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase  
protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1  
45 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a  
BAC end sequence (GSS), complete sequence.//9.7e-144:809:87//AL021068
- 50 F-HEMBB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic  
sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.12:492:58//AC004157
- F-HEMBB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic  
sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0024:212:67//AC004157
- 55 F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds.//1.5e-32:200:94//AF085351



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F-HEM BB1000883//HS\_3065\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3065 Col=8 Row=F, genomic survey sequence.//0.0017:  
152:66//AQ137687

5

F-HEM BB1000887

F-HEM BB1000888//CIT-HSP-2329A10.TR CIT-HSP Homo sapiens genomic clone 2329A10,  
10 genomic survey sequence.//1.5e-31:172:98//AQ044369

F-HEM BB1000890

15 F-HEM BB1000893//Plasmodium falciparum MAL3P2, complete sequence.//9.5e-06:768:  
56//AL034558

20 F-HEM BB1000908//Homo sapiens clone DJ1119N05, complete sequence.//4.5e-21:199:  
82//AC004968

F-HEM BB1000910//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
MAL4P1, WORKING DRAFT SEQUENCE.//0.72:366:59//AL034557

25

F-HEM BB1000913//HS\_3078\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-  
12:221:63//AQ144507

30

F-HEM BB1000915//Homo sapiens DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate  
P4.//1.2e-49:252:99//AJ001215

35 F-HEM BB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete  
sequence.//2.3e-42:316:76//AC006077

40 F-HEM BB1000927//Human BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30:528:  
65//D16593

F-HEM BB1000947//CpG0856B CplOWAgDNA1 Cryptosporidium parvum genomic, genomic  
survey sequence.//0.81:262:62//AQ254493

45

F-HEM BB1000959//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
346O6, WORKING DRAFT SEQUENCE.//1.2e-43:454:75//Z84487

50 F-HEM BB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds.//8.3e-42:458:  
72//AF099973

55 F-HEM BB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5,  
complete sequence.//0.98:196:63//AB005234

F-HEM BB1000981

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- 5 F-HEM BB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//AC004476
- F-HEM BB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//0.099:391:57//Z98753
- 10 F-HEM BB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//6.2e-33:227:80//Z94802
- 15 F-HEM BB1001004
- F-HEM BB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:79//AC002551
- 20 F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:69//AC002310
- 25 F-HEM BB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:58//AC005751
- 30 F-HEM BB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.6e-39:218:80//AF069291
- F-HEM BB1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717
- 35 F-HEM BB1001037//CIT-HSP-2358K16.TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey sequence.//6.6e-05:228:64//AQ080539
- 40 F-HEM BB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//4.0e-27:385:71//U82671
- F-HEM BB1001051//H.sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586
- 45 F-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-89:180:91//AC006014
- 50 F-HEM BB1001058//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006060
- 55 F-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//U49973
- F-HEM BB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING DRAFT SEQUENCE.//7.1e-162:770:99//AL034375

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- 5 F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803
- 10 F-HEMBB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210
- 15 F-HEMBB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612
- 20 F-HEMBB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987
- 25 F-HEMBB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630
- 30 F-HEMBB1001114//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//7.2e-07:459:59//AC005284
- 35 F-HEMBB1001117//HS\_2178\_B1\_E12\_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244
- 40 F-HEMBB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:98//U73778
- 45 F-HEMBB1001126
- 50 F-HEMBB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673
- 55 F-HEMBB1001137
- 60 F-HEMBB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617
- 65 F-HEMBB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264
- 70 F-HEMBB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724
- 75 F-HEMBB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-

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63:259:79//AL008712

- 5 F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334
- F-HEMBB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 2321I17, genomic survey sequence.//5.9e-27:320:75//AQ036473
- 10 F-HEMBB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//5.7e-06:62:96//B85188
- F-HEMBB1001199
- 15 F-HEMBB1001208//HS\_2026\_B1\_C07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237
- 20 F-HEMBB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357
- 25 F-HEMBB1001210//HS\_3102\_A2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196
- 30 F-HEMBB1001218//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291
- 35 F-HEMBB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504
- F-HEMBB1001234//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39f9, forward read cpg39f9.ft1e//4.0e-30:171:97//Z65435
- 40 F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754
- 45 F-HEMBB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087
- 50 F-HEMBB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032
- F-HEMBB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173
- 55 F-HEMBB1001267//Homo sapiens chromosome 17, clone hRPK.488\_L\_1, complete sequence.//3.5e-30:236:78//AC005303

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- 5 F-HEMBB1001271//HS\_3011\_A1\_G02\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-  
07:364:62//AQ214217
- 10 F-HEMBB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20;  
genomic survey sequence.//1.8e-16:109:97//AQ060969
- F-HEMBB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366
- 15 F-HEMBB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:  
434:74//AC000387
- 20 F-HEMBB1001294//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-  
90:437:99//AQ155035
- F-HEMBB1001302
- 25 F-HEMBB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15,  
genomic survey sequence.//2.2e-07:370:61//B69144
- 30 F-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA,  
complete cds.//5.7e-116:663:85//U92703
- 35 F-HEMBB1001315//Homo sapiens chromosome 10 clone LA10NC01\_40\_G\_3 map  
10q26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:  
77//AC006096
- 40 F-HEMBB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human  
BAC Library) complete sequence.//1.4e-122:680:91//AC006210
- F-HEMBB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete  
sequence.//2.8e-09:518:60//AC004129
- 45 F-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds,  
strain:BALB/c.//3.7e-56:458:79//D63850
- 50 F-HEMBB1001335//HS\_3055\_A1\_H10\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3055 Col=19 Row=O, genomic survey sequence.//1.0:  
222:63//AQ147384
- 55 F-HEMBB1001337//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.0e-74:  
319:85//AC003983
- F-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.0e-

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135:856:87//U85056

5 F-HEMBB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds.//3.3e-44:481:74//U50871

10 F-HEMBB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//1.8e-17:210:73//AC006041

F-HEMBB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:386:59//AC005079

15 F-HEMBB1001364//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//0.97:349:61//AC004662

20 F-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence.//5.5e-161:766:98//AC005876

25 F-HEMBB1001367//Homo sapiens chromosome 17, clone hRPC.906\_A\_24, complete sequence.//3.0e-55:510:76//AC004408

F-HEMBB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.//0.048:244:64//AC005192

30 F-HEMBB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//2.5e-26:257:78//AC006204

35 F-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//5.1e-99:571:89//AF071314

40 F-HEMBB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//7.1e-05:546:58//X02354

F-HEMBB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//4.0e-129:788:88//AC005023

45 F-HEMBB1001410//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.8e-11:632:59//AF045555

50 F-HEMBB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequence.//0.0012:435:59//AC003019

55 F-HEMBB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.8e-17:360:64//AC005482

F-HEMBB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt.//4.1e-114:668:88//S65367

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- 5 F-HEM BB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.3e-37:438:74//AB000931
- F-HEM BB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds.//9.1e-92:550:88//L18966
- 10 F-HEM BB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142), complete sequence.//0.00024:385:62//AC004768
- 15 F-HEM BB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//AC005790
- 20 F-HEM BB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//8.0e-40:377:78//AC000382
- F-HEM BB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.011:482:59//AF001549
- 25 F-HEM BB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263:61//U91320
- 30 F-HEM BB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521:66//U92564
- 35 F-HEM BB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-31:479:71//AC004873
- F-HEM BB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-51:680:70//AC005080
- 40 F-HEM BB1001527
- F-HEM BB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR Region, complete sequence.//1.3e-79:696:79//AC000089
- 45 F-HEM BB1001535//O.aries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217:62//X89268
- 50 F-HEM BB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266:60//AC004548
- 55 F-HEM BB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//AC004262
- F-HEM BB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7,

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complete sequence.//6.9e-50:213:80//AC004605

5 F-HEMBB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041

10 F-HEMBB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989

15 F-HEMBB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//AC004003

20 F-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-166:816:97//AL031677

25 F-HEMBB1001586

30 F-HEMBB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//AC005261

35 F-HEMBB1001603

40 F-HEMBB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422:72//Z99289

45 F-HEMBB1001619//HS\_3079\_B1\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388

50 F-HEMBB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:667:59//AC005089

55 F-HEMBB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475:57//AL034559

60 F-HEMBB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168:76//AL021155



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F-HEMBB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.00097:721:58//AB006702

5 F-HEMBB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//0.15:276:63//AC002038

10 F-HEMBB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393:61//L14320

15 F-HEMBB1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275:60//B12308

F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546

20 F-HEMBB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//86429

25 F-HEMBB1001685//CIT-HSP-2287O9.TF CIT-HSP Homo sapiens genomic clone 2287O9, genomic survey sequence.//2.3e-34:191:97//B99261

30 F-HEMBB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178

35 F-HEMBB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575

40 F-HEMBB1001706

F-HEMBB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543

45 F-HEMBB1001717//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.1e-13:723:58//AJ223323

50 F-HEMBB1001735//Human PAC clone DJ0596O09 from 7p15, complete sequence.//1.3e-36:427:73//AC003074

F-HEMBB1001736//S.pombe chromosome II cosmid c4B4.//0.0085:479:57//AL023706

55 F-HEMBB1001747//Homo sapiens PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376

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F-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.3e-98:395:82//AC005829

5 F-HEM BB1001753//S.maximus repeat region, 342bp.//4.2e-11:69:85//Z78099

F-HEM BB1001756//Homo sapiens full-length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064

10

F-HEM BB1001760//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275

15 F-HEM BB1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184

20 F-HEM BB1001785//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746

F-HEM BB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272

25 F-HEM BB1001802//Plasmodium falciparum MAL3P7, complete sequence.//1.8e-11:538:60//AL034559

30 F-HEM BB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882

35 F-HEM BB1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204

F-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209

40 F-HEM BB1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 2291012, genomic survey sequence.//7.6e-08:73:94//AQ004168

45 F-HEM BB1001836//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801

F-HEM BB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073

50 F-HEM BB1001850//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504

55 F-HEM BB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581

F-HEM BB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and

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exons 2-10, complete cds.//1.7e-56:399:86//U07563

- 5 F-HEMBB1001868//Rattus norvegicus clone 923 polymeric immunoglobulin receptor mRNA  
3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet  
repeats.//6.1e-08:234:67//U01145
- 10 F-HEMBB1001869//Homo sapiens full-length insert cDNA clone YT86F01.//7.4e-87:432:  
97//AF085974
- F-HEMBB1001872
- 15 F-HEMBB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//3.4e-14:631:61//AC005000
- 20 F-HEMBB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT  
SEQUENCE.//0.93:415:57//Z82209
- 25 F-HEMBB1001880//Human genomic DNA sequence from clone 308O1 on chromosome  
Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403
- F-HEMBB1001899//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
contig 4-10, complete sequence.//0.0038:425:58//AL010216
- 30 F-HEMBB1001905//S.pombe chromosome III cosmid c330.//1.1e-23:520:62//AL031603
- F-HEMBB1001906
- 35 F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete  
cds.//3.7e-82:672:81//U47742
- 40 F-HEMBB1001910//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505
- 45 F-HEMBB1001911//Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence,  
complete sequence.//1.0:581:58//AC004705
- F-HEMBB1001915//Caenorhabditis elegans cosmid T05H10, complete sequence.//1.2e-16:  
283:67//Z47812
- 50 F-HEMBB1001921//Homo sapiens chromosome 17, clone hCIT.123\_J\_14, complete  
sequence.//3.4e-07:803:58//AC003950
- 55 F-HEMBB1001922//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete  
sequence.//5.0e-06:756:56//AE001391
- F-HEMBB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35.

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Contains delta opiate receptor, CpG island, CA repeat.//3.1e-45:609:73//AL009181

- 5 F-HEM BB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of  
hepatocellular colorectal and non-small cell lung cancer , segment 10/11.//3.2e-158:745:  
99//AB020867
- 10 F-HEM BB1001944//, complete sequence.//4.1e-60:638:73//AC005815
- F-HEM BB1001945//HS\_3185\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:  
280:58//AQ188882
- 15 F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:333:  
66//AB002390
- 20 F-HEM BB1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:180:63//M62899
- F-HEM BB1001952//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341
- 25 F-HEM BB1001953//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete  
sequence.//0.11:589:58//AC005284
- 30 F-HEM BB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains  
exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion  
channel, ESTs, CpG island.//9.8e-25:446:67//Z98941
- 35 F-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete  
sequence.//2.8e-147:727:97//AC005736
- 40 F-HEM BB1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15  
unordered pieces.//3.2e-56:650:71//AC004963
- F-HEM BB1001973//Homo sapiens chromosome 12p13.3-clone RPC111-350L7, WORKING  
DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844
- 45 F-HEM BB1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4,  
genomic survey sequence.//8.8e-35:198:96//AQ028071
- 50 F-HEM BB1001988//D.polychroa microsatellite sequence (clone Dp 1C e12).//4.5e-07:337:  
62//X92189
- 55 F-HEM BB1001990//HS\_3234\_A1\_G08\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:  
279:59//AQ204689

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F-HEMBB1001996//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507

5 F-HEMBB1001997//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069

10 F-HEMBB1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153

15 F-HEMBB1002005//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685

F-HEMBB1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506

20 F-HEMBB1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05 :126:76//AP000056

25 F-HEMBB1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012

F-HEMBB1002043

30 F-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-167:809:97//AC005740

35 F-HEMBB1002045

F-HEMBB1002049//Homo sapiens chromosome 17, clone hRPC.161\_P\_9, complete sequence.//0.87:177:65//AC006237

40 F-HEMBB1002050//Streptomyces coelicolor cosmid D78.//8.5e-08:644:58//AL034355

45 F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512

F-HEMBB1002069

50 F-HEMBB1002092//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B331O8; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064

55 F-HEMBB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476

F-HEMBB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete

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sequence.//0.00023:542:61//AC004035

- 5 F-HEMBB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843
- 10 F-HEMBB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714
- 15 F-HEMBB1002142//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748
- F-HEMBB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421
- 20 F-HEMBB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998
- 25 F-HEMBB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140
- F-HEMBB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80846
- 30 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:405:67//X52332
- F-HEMBB1002218//HS\_2056\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711
- 35 F-HEMBB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648
- 40 F-HEMBB1002247
- 45 F-HEMBB1002249//Homo sapiens DNA sequence from BAC 34I8 on chromosome 6p21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-45:327:83//AL021918
- 50 F-HEMBB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506
- 55 F-HEMBB1002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035:312:62//Z98547

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- 5 F-HEM BB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//AC005504
- F-HEM BB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//5.3e-18:527:61//AC004682
- 10 F-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//8.6e-139:818:88//U73642
- 15 F-HEM BB1002306//HS\_3109\_A2\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=O, genomic survey sequence.//1.3e-75:371:98//AQ148164
- 20 F-HEM BB1002327//HS\_3235\_B2\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence.//3.3e-83:418:97//AQ209752
- 25 F-HEM BB1002329//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402
- F-HEM BB1002340
- 30 F-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//4.1e-154:724:98//AJ010841
- 35 F-HEM BB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3e-36:192:98//L16991
- 40 F-HEM BB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//1.8e-13:96:96//U55766
- F-HEM BB1002364//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946
- 45 F-HEM BB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-06:674:56//AC004153
- 50 F-HEM BB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222
- F-HEM BB1002383
- 55 F-HEM BB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 2173E20, genomic survey sequence.//5.2e-17:434:66//B91052

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F-HEMBB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712

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F-HEMBB1002415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//8.9e-35:334:75//AL031319

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F-HEMBB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//U62317

15

F-HEMBB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//U92010

20

F-HEMBB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING DRAFT SEQUENCE.//2.7e-43:419:78//AL034349

F-HEMBB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.3e-27:542:68//AC005534

25

F-HEMBB1002458//HS\_3246\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993

30

F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885

35

F-HEMBB1002489

F-HEMBB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919

40

F-HEMBB1002495//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//1.1e-16:297:68//AC006141

45

F-HEMBB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-91:675:82//AC005230

F-HEMBB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//2.7e-11:648:60//AC004605

50

F-HEMBB1002510//HS\_3236\_B1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3236 Col=21 Row=P, genomic survey sequence.//1.2e-06:67:94//AQ205992

55

F-HEMBB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequence.//1.2e-70:580:72//AC006152



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F-HEMBB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Systems Human BAC library) complete sequence.//5.6e-22:516:64//AC004553 F-HEMBB1002531

5 F-HEMBB1002534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//6.9e-62:265:87//AL034346

10 F-HEMBB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequence.//2.7e-44:200:82//AC000059

15 F-HEMBB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, complete sequence.//0.22:161:68//AC004927

F-HEMBB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//7.5e-43:306:77//AC004861

20 F-HEMBB1002579

25 F-HEMBB1002582//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.00018:431:61//AL033520

F-HEMBB1002590//Yeast (S.cerevisiae) mitochondrial apocytochrome b gene, 3' flank.//0.78:147:64//J01471

30 F-HEMBB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 9E21, WORKING DRAFT SEQUENCE.//3.6e-50:692:69//AL008639

35 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749

40 F-HEMBB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//1.5e-07:416:60//AC002381

F-HEMBB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454

45 F-HEMBB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, complete cds.//0.0042:460:60//AF009614

50 F-HEMBB1002610//Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-23:559:63//AC003029

55 F-HEMBB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//AC000025

F-HEMBB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:324:56//AE001417

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- 5 F-HEMBB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:441:60//AF001550
- F-HEMBB1002623//C.hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304
- 10 F-HEMBB1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//U34819
- 15 F-HEMBB1002664//HS\_2265\_A1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2265 Col=11 Row=O, genomic survey sequence.//0.54:115:67//AQ101557
- 20 F-HEMBB1002677//Homo sapiens (subclone 3\_d1 from P1 H25) DNA sequence, complete sequence.//2.2e-49:784:68//L81774
- F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23.//1.0:112:63//U04492
- 25 F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 772 Col=12 Row=M, genomic survey sequence.//4.4e-07:86:84//B39748
- 30 F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=20 Row=L, genomic survey sequence.//0.98:183:61//B34077
- 35 F-HEMBB1002692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE.//0.00039:408:60//AL033525
- 40 F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.3e-35:323:74//AC004955
- 45 F-HEMBB1002699//Mus musculus D6MM5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and LOR2 protein (Lor2) gene, partial cds.//0.031:325:62//AF084363
- 50 F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=2 Row=G, genomic survey sequence.//1.8e-25:158:95//B34720
- 55 F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//1.7e-137:534:96//AB003151
- F-HEMBB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//0.0019:612:58//Z71187

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- 5 F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING  
DRAFT SEQUENCE, 3 unordered pieces.//6.1e-43:354:81//AC003117
- F-MAMMA1000019
- 10 F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//2.0e-  
40:185:97//Z47553
- F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete  
sequence.//1.0:211:65//AC005483
- 15 F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12.//0.075:  
204:65//M73275
- 20 F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2  
Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted  
repeat, complete sequence.//4.1e-122:495:79//AL031073
- 25 F-MAMMA1000055//M.musculus mRNA for testin.//2.1e-35:559:66//X78989
- F-MAMMA1000057//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete  
sequence.//5.5e-121:703:89//AC005829
- 30 F-MAMMA1000069//Homo sapiens minisatellite ceb1 repeat region.//0.00013:329:  
60//AF048727
- 35 F-MAMMA1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome  
Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.1e-53:445:79//Z93023
- 40 F-MAMMA1000085//Caenorhabditis elegans cosmid Y23H5A.//0.0017:164:64//AF077541
- F-MAMMA1000092//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete  
sequence.//1.2e-70:598:78//AC004744
- 45 F-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete  
sequence.//1.1e-156:857:92//AC003976
- 50 F-MAMMA1000117//HS\_3223\_B2\_D08\_T7 CIT. Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3223 Col=16 Row=H, genomic survey sequence.//5.4e-  
100:527:94//AQ221160
- 55 F-MAMMA1000129//ryanodine receptor.//0.055 :492:59//A20359
- F-MAMMA1000133

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F-MAMMA1000134//HS\_3078\_B1\_C02\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//2.1e-  
93:462:97//AQ144362

5

F-MAMMA1000139//Homo sapiens Xp22 PAC RPCI1-5G11 (from Roswell Park Cancer  
Center) complete sequence.//3.3e-14:322:65//AC002369

10

F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds.//6.9e-25:148:  
97//AB014585

15

F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA,  
complete cds.//1.0e-29:219:87//AF031924

F-MAMMA1000163

20

F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete  
sequence.//6.3e-14:92:88//AC005393

25

F-MAMMA1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds.  
similar to Human Drebrin.//2.2e-114:698:87//U58884

30

F-MAMMA1000175//HS\_3050\_B1\_B03\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3050 Col=5 Row=D, genomic survey sequence.//6.2e-  
73:357:99//AQ102678

35

F-MAMMA1000183//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
Y313F4, WORKING DRAFT SEQUENCE.//4.6e-94:904:73//AL023808

F-MAMMA1000198//Z.diploperennis repetitive DNA (clone ZEAR 266).//0.18:152:70//X53610

40

F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete  
sequence.//0.017:99:75//AC004583

45

F-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
467K16, WORKING DRAFT SEQUENCE.//0.36:312:62//AL031283

50

F-MAMMA1000241//HS\_3217\_B1\_B02\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-  
94:456:98//AQ193401

F-MAMMA1000251//Homo sapiens NF2 gene.//0.00092:270:64//Y18000

55

F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic  
sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC005140

F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome

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6p22.1-22.3. Contains EST and STS.//0.00036:230:65//AL022717

5 F-MAMMA1000264//Homo sapiens (subclone 9\_f5 from P1 H17) DNA sequence, complete sequence.//1.5e-30:499:68//L81612

10 F-MAMMA1000266//Bacillus lynceorum strain pMEL12 Bag320 satellite DNA.//0.28:218:64//AF034430

F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.4e-157:788:96//AF001549

15 F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.//0.70:320:61//AL021897

20 F-MAMMA1000278//Sequence 23 from patent US 5708157.//9.3e-103:540:95//80055

F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS, GSS, complete sequence.//2.4e-49:262:77//AL031643

25 F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//1.1e-30:324:75//B03004

30 F-MAMMA1000287//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//2.7e-54:401:83//AC006213

35 F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541

40 F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPCI5-1154L15, WORKING DRAFT SEQUENCE, 67 unordered pieces.//0.15:449:59//AC006205

F-MAMMA1000309//cDNA coding human apolipoprotein E3.//0.00010:691:58//E00359

45 F-MAMMA1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 798A17, WORKING DRAFT SEQUENCE.//0.27:301:60//AL031274

F-MAMMA1000313

50 F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:71//AC002400

55 F-MAMMA1000339

F-MAMMA1000340//HS\_2181\_B2\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-

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05:181:68//AQ024288

5 F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//5.3e-30:575:66//AC004139

10 F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-52:264:76//AC005052

F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//6.5e-91:569:88//AC004879

15 F-MAMMA1000361//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950

20 F-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//2.9e-114:516:89//AL022345

25 F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//6.9e-26:377:71//AQ279944

30 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:98//AB015132

F-MAMMA1000395

35 F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence.//4.0e-115:845:85//AC005999

40 F-MAMMA1000410//HS\_3245\_A1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=3 Row=E, genomic survey sequence.//9.6e-42:350:80//AQ205768

45 F-MAMMA1000413//HS\_3223\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey sequence.//1.6e-48:318:89//AQ188456

50 F-MAMMA1000414//HS\_2027\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence.//1.4e-46:286:92//AQ231369

55 F-MAMMA1000416//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004640

F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence.//3.3e-29:223:84//AC005630

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F-MAMMA1000422

5 F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule.//2.2e-10:639:57//X03240

10 F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.6e-47:556:68//AC003973

F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//8.0e-99:545:92//AF062484

15 F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-41:289:79//AC005283

20 F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and ESTs, complete sequence.//2.3e-34:291:80//Z99755

25 F-MAMMA1000446

F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence.//5.0e-53:231:84//AF046620

30 F-MAMMA1000468//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.75:303:60//Z93017

35 F-MAMMA1000472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543

40 F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.5e-54:369:77//AC005081

F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//3.6e-34:332:77//AC004381

45 F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPC11-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//8.9e-128:822:87//AC003686

50 F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 2319O5, genomic survey sequence.//4.8e-29:175:94//AQ044812

55 F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//5.7e-45:334:82//AL022336

F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains

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ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATP5G2, ATP5G3)  
like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.9e-43:529:69//Z92545

- 5 F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2  
Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST,  
CA repeat, STS, CpG island, complete sequence.//2.0e-14:380:63//AL022576
- 10 F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-  
10p12.1, complete sequence.//1.4e-22:420:66//AC006101
- F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08.//5.4e-29:168:97//D16922
- 15 F-MAMMA1000565//RPCI11-61K6.TJ RPCI11 Homo sapiens genomic clone R-61K6,  
genomic survey sequence.//1.7e-120:561:100//AQ194238
- 20 F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS6791  
and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG  
island.//3.1e-43:387:80//Z81370
- 25 F-MAMMA1000576//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.2e-  
30:237:75//AC005104
- F-MAMMA1000583//RPCI11-60M22.TJ RPCI11 Homo sapiens genomic clone R-60M22,  
30 genomic survey sequence.//9.6e-102:487:99//AQ198091
- F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete  
sequence.//5.2e-39:370:78//AC006195
- 35 F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete  
sequence.//3.9e-43:328:83//AC005338
- 40 F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete  
sequence.//1.5e-32:259:82//AC005839
- 45 F-MAMMA1000605//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
97P20, WORKING DRAFT SEQUENCE.//2.4e-59:318:83//AL031297
- F-MAMMA1000612//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-  
50 30:171:96//AQ116793
- F-MAMMA1000616//HS\_3176\_A1\_E06\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-  
55 28:287:79//AQ300310
- F-MAMMA1000621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone



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273F20, WORKING DRAFT SEQUENCE.//0.015:478:58//AL034371

F-MAMMA1000623

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F-MAMMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196:61//E06898

F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds.//0.95:365:  
59//AF023674

10

F-MAMMA1000664//HS\_3096\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-  
51:257:99//AQ145137

15

F-MAMMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete  
sequence.//2.0e-66:586:67//AC004785

20

F-MAMMA1000670//HS\_2243\_B2\_A08\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence.//8.7e-  
05:94:80//AQ153650

25

F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.9e-64:471:  
81//AF046705

30

F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:186:67//U27489

F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2;  
neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2;  
ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-  
2.//3.0e-53:653:70//L05367

35

F-MAMMA1000707//CIT-HSP-2302019.TR CIT-HSP Homo sapiens genomic clone 2302019,  
genomic survey sequence.//1.8e-08:131:77//AQ017947

40

F-MAMMA1000713//Rattus norvegicus clonel polymeric immunoglobulin receptor mRNA 3'  
untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet  
repeats.//0.062:134:67//U00762

45

F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.//1.0:266:  
61//X15028

50

F-MAMMA1000718//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10,  
genomic survey sequence.//3.6e-05:289:60//B95401

55

F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete  
sequence.//4.4e-184:842:98//AC005781

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F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-05:430:60//AC004917

5 F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//3.8e-55:796:66//AC004274

10 F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:555:74//AF064859

15 F-MAMMA1000733//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479:58//AL031749

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168:802:98//AF100141

20 F-MAMMA1000738//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-31:626:63//Z71408

25 F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410:82//X06123

30 F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence.//3.7e-109:779:83//AC004158

F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444:63//AC005075

35 F-MAMMA1000760//Homo sapiens clone RG015P03, complete sequence.//1.5e-44:403:79//AC005048

40 F-MAMMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159:81//AC004166

45 F-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.3e-51:789:68//AC005703

F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//5.7e-40:238:78//Z95116

50 F-MAMMA1000778//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222:84//AL031118

55 F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9.//0.90:137:62//U94987

F-MAMMA1000798//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6,

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B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.00058:163:71//AC003656

5

F-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//6.3e-151:714:99//AC005339

10

F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912

15

F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0.76:302:58//AC005502

20

F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456

F-MAMMA1000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755

25

F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817

30

F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710

F-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557

35

F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146

40

F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10.//0.081:229:62//M30549

45

F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747

50

F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553

F-MAMMA1000862

F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050

55

F-MAMMA1000865

F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8,

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genomic survey sequence.//0.00017:158:70//AQ240906

5 F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152

10 F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152

15 F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336

20 F-MAMMA1000880//Homo sapiens full-length insert cDNA clone ZD54A10.//5.2e-26:143:100//AF086327

F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801

25 F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y11283

30 F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433

35 F-MAMMA1000906//HS\_3110\_B2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819

F-MAMMA1000908//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397

40 F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560

45 F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//889575

50 F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917

55 F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296

F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299

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- 5 F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23  
Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete  
sequence.//1.8e-14:175:76//AL031117
- 10 F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308
- 15 F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete  
sequence.//3.3e-30:530:67//AC004643
- 20 F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//1.8e-58:318:86//AC006001
- 25 F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome  
20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-  
Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-  
Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable  
30 Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains  
a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:  
65//AL022394
- 35 F-MAMMA1000975//Human DNA sequence from clone 344I7 on chromosome Xp11.21-11.3.  
Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and  
a GSS, complete sequence.//1.4e-79:690:77//AL024458
- 40 F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete  
sequence.//0.089:214:66//AC004991
- 45 F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:  
458:82//AC000114
- F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12.  
Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406
- 50 F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21.  
Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB  
proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochochoidal  
Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:  
55 68//AL022401
- F-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT

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SEQUENCE.//1.6e-103:139:99//AJ011929

- 5 F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567
- 10 F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701
- 15 F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:6//1AF061444
- 20 F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990
- F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903
- 25 F-MAMMA1001041//chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597
- F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457
- 30 F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125
- 35 F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169
- 40 F-MAMMA1001073//HS\_3046\_A2\_G08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420
- F-MAMMA1001074//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733
- 45 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749
- 50 F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//2.0e-22:334:69//AC006120
- 55 F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155
- F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087

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- 5 F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05 :594:60//AC005256
- F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019
- 10 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045
- 15 F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637
- F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825
- 20 F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116
- 25 F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//1.6e-84:406:82//S70011
- 30 F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//1.3e-14:182:76//AL022339
- F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//5.2e-87:714:78//Z71187
- 35 F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13 genomic survey sequence.//0.00051:249:61//AQ055735
- 40 F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//2.2e-30:410:70//AC004518
- 45 F-MAMMA1001162//Homo sapiens full-length insert cDNA clone ZA79C01.//2.4e-13:87:100//AF086123
- 50 F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds.//9.3e-15:432:60//U31629
- F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//6.8e-57:670:72//AC005696
- 55 F-MAMMA1001191
- F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//1.5e-117:759:84//U29156

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F-MAMMA1001202

- 5 F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.5e-161:764:98//AC005412
- 10 F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//5.1e-30:535:65//AC004099
- 15 F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//8.4e-182:860:98//AC005393
- 20 F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.7e-58:690:70//AC004875
- 25 F-MAMMA1001222//Mouse loricrin mRNA, complete cds.//2.7e-07:624:58//M34398
- 30 F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.91:177:66//AC005726
- 35 F-MAMMA1001244
- 40 F-MAMMA1001249//Human 28S ribosomal RNA psuedogenes and alu repeat region sequence.//6.7e-09:502:58//U67616
- 45 F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//5.0e-37:342:80//Z99495
- 50 F-MAMMA1001259
- 55 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//8.7e-40:659:64//AB014561
- 60 F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//4.9e-43:265:81//AC004453
- 65 F-MAMMA1001271//Salmo salar DNA for a cryptic repeat.//2.6e-06:311:63//AJ012206
- 70 F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.6e-70:327:83//AC004840
- 75 F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-05 :276:66//AC003035
- 80 F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class



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A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//3.6e-98:199:98//AL022314

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F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38B4, genomic survey sequence.//4.7e-33:292:71//AQ030084

10

F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.6e-182:860:98//AC005703

15

F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.9e-70:163:97//Z93244

20

F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence.//2.6e-19:379:68//AL031290

25

F-MAMMA1001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 197L1, WORKING DRAFT SEQUENCE.//4.5e-131:751:90//AL031390

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F-MAMMA1001330

F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906

35

F-MAMMA1001343//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744

F-MAMMA1001346

40

F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.0e-44:505:74//AC004086

45

F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a mRNA, complete cds.//1.5e-07:415:58//M86826

50

F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.21-12.1 Contains EST, STS and GSS, complete sequence.//1.6e-23 :209:75//AL022332

55

F-MAMMA1001408//HS\_3242\_A1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=O, genomic survey sequence.//2.7e-07:181:69//AQ207300

F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II

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protein (PKD2) gene, exon 14.//0.98:120:68//AF004872

5 F-MAMMA1001419//HS\_2053\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-  
75 :424:93//AQ244585

10 F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete  
sequence.//2.4e-09:199:70//AC004049

15 F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4,  
WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529 F-  
MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete  
sequence.//0.0019:516:56//AE001400

20 F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC  
library) complete sequence.//3.6e-42:486:70//AC003684

25 F-MAMMA1001452//RPC11-48022.TJ RPC11 Homo sapiens genomic clone R-48O22,  
genomic survey sequence.//5.3e-87:423:98//AQ199294

F-MAMMA1001465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543

30 F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:  
87//L31783

35 F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//1.0e-13:158:77//AC005486

40 F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit  
(muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366

F-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714

45 F-MAMMA1001510//Human PAC clone DJ438O4 from 22q12.1-qter, complete  
sequence.//1.1e-05:371:61//AC002378

50 F-MAMMA1001522

F-MAMMA1001547

55 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:  
98//AB007931

F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete

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sequence.//0.97:154:68//AF001548

- 5 F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//M61764
- F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12  
Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete  
sequence.//1.8e-07:104:84//Z98949
- 10 F-MAMMA1001600//HS\_3022\_A2\_H01\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3022 Col=2 Row=O, genomic survey sequence.//1.6e-  
66:405:90//AQ163791
- 15 F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25  
Contains EST, CA repeat, Ninenin like sequence, complete sequence.//0.00043:715:  
58//AL008626
- 20 F-MAMMA1001606//Jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei  
genomic clone 2G6, genomic survey sequence.//0.19:266:62//B13685
- 25 F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete  
cds.//9.7e-54:442:69//AF053630
- 30 F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive  
site.//0.14:221:62//M29833
- F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING  
DRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412
- 35 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:  
67//U57796
- 40 F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete  
sequence.//4.0e-35:407:70//AC000118
- 45 F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2.  
Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated,  
actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S  
Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete  
sequence.//0.44:245:63//AL022577
- 50 F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284
- 55 F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16,  
genomic survey sequence.//9.7e-05:146:66//B95491
- F-MAMMA1001670//HS\_3136\_A1\_G06\_MR CIT Approved Human Genomic Sperm Library D

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Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779

5 F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614

10 F-MAMMA1001679//HS\_3054\_A1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=O, genomic survey sequence.//1.0:89:70//AQ106118

15 F-MAMMA1001683//Spermatozopsis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970

20 F-MAMMA1001686//HS\_3219\_B1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345

25 F-MAMMA1001692//HS\_3047\_B1\_B10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228

30 F-MAMMA1001711//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-42:316:82//AC004845

F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125

35 F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687

40 F-MAMMA1001735//chicken brain tubulin beta chain mrna.//3.5e-110:740:84//J00913

F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001

45 F-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//3.2e-16:194:75//AC006017

50 F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998

55 F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718

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- 5 F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds.//1.2e-35:583:65//U90065
- 10 F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338
- 15 F-MAMMA1001757//HS\_2058\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865
- 20 F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6.6e-76:349:87//AL022722
- 25 F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.23:633:57//M97514
- F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801
- 30 F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801
- 35 F-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.7e-106:744:82//X85991
- F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563
- 40 F-MAMMA1001785
- 45 F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence.//5.0e-05:152:74//Z99129
- 50 F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845
- 55 F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262
- F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383

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- 5 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128
- 10 F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031
- 15 F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.71:179:67//AJ011930
- 20 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79//Y13148
- 25 F-MAMMA1001824//HS\_3108\_A1\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508
- 30 F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537\_E\_1, complete sequence.//3.4e-45:312:85//AC006211
- 35 F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042
- 40 F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo sapiens genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620
- 45 F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmid R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390
- 50 F-MAMMA1001854
- 55 F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11L22, genomic survey sequence.//0.091:161:65//B75631
- F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013
- F-MAMMA1001868//HS\_2196\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455
- F-MAMMA1001874//H.sapiens CpG island DNA genomic Mse1 fragment, clone 63h5, reverse read cpg63h5.rta.//1.0:127:63//Z62129
- 55 F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802

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F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465

5 F-MAMMA1001890//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707

10 F-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207

15 F-MAMMA1001908//HS\_2225\_A1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey sequence.//5.4e-08:264:62//AQ301597

20 F-MAMMA1001931//HS\_3049\_B2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157

F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493

25 F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656

30 F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//5.3e-63:479:78//Z73986

35 F-MAMMA1001970//Homo Sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071

40 F-MAMMA1001992//HS\_3078\_A1\_A09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646

45 F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214\_O\_I, complete sequence.//1.5e-07:244:62//AC005224

50 F-MAMMA1002011//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711

F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803

55 F-MAMMA1002033//HS\_3023\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493

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- 5 F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227
- 10 F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//1.4e-20:314:70//AC005669
- 15 F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPCII1-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906
- 20 F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996
- 25 F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869
- 30 F-MAMMA1002068//Homo sapiens, clone hRPK.2\_A\_1, complete sequence.//5.4e-41:407:78//AC006197
- 35 F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313
- 40 F-MAMMA1002082
- 45 F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380
- 50 F-MAMMA1002093//HS\_3050\_B1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997
- 55 F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//8.3e-10:464:60//AF017308
- F-MAMMA1002118
- F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962
- F-MAMMA1002132//RPCI11-78F11.TJ RPCI11 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460



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F-MAMMA1002140//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216

5 F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338

10 F-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391

15 F-MAMMA1002153//HS\_3005\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213

20 F-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431

F-MAMMA1002156

25 F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165

30 F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448

F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212

35 F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548

40 F-MAMMA1002209//HS\_2197\_B1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058

45 F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//6.3e-08:435:60//AF017308

50 F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.8e-124:752:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC004710

55 F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253

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F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.4e-145:691:98//AC005666

5 F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600

10 F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence.//0.066:333:60//AC003676

15 F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.1e-39:404:74//AF068748

20 F-MAMMA1002269//HS\_3163\_B1\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=5 Row=H, genomic survey sequence.//1.0:150:63//AQ171576

25 F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.5e-22:315:67//AC003108

30 F-MAMMA1002292//B.garinii (strain Tls1) p83/100 gene (partial).//0.73:200:64//X81533

35 F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//1.6e-56:408:75//AC006023

40 F-MAMMA1002294//Sequence 2 from Patent WO9516779.//1.8e-06:401:62//A45258

45 F-MAMMA1002297

50 F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:525:61//AC004221

55 F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey sequence.//1.2e-90:446:98//AQ053994

60 F-MAMMA1002308//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.3e-35:329:78//AL031680

65 F-MAMMA1002310//Human gastric (H<sup>+</sup> → K<sup>+</sup>) ATPase gene, complete cds.//0.0060:301:60//J05451

70 F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737

75 F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25.

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Contains ESTs and STS.//1.3e-09:741:58//Z86064

- 5 F-MAMMA1002317
- F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//AC005756
- 10 F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:617:70//AC004796
- 15 F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//U93871
- 20 F-MAMMA1002332//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//1.6e-31:287:74//AL034402
- F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//AL022022
- 25 F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases 1.41604.//2.1e-57:522:77//AJ011932
- 30 F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//AC004129
- 35 F-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORKING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100
- F-MAMMA1002352//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING DRAFT SEQUENCE.//5.8e-17:326:70//Z98742
- 40 F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.1e-14:399:63//AC004825
- 45 F-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING DRAFT SEQUENCE.//3.7e-43:420:75//AL023879
- 50 F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153
- F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.3e-18:156:75//AC005831
- 55 F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.//4.9e-43:353:69//Z68885

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F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//1.8e-22:282:74//AL008719

5 F-MAMMA1002362//Platemys spixii CR1-like LINE, partial sequence.//0.00058:83:79//D82938

F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey sequence.//4.4e-10:85:92//AQ196889

10

F-MAMMA1002384//RPC111-80J20.TV RPC111 Homo sapiens genomic clone R-80J20, genomic survey sequence.//2.7e-56:286:98//AQ284134

15 F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey sequence.//5.5e-46:335:84//AQ043985

20 F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-29:273:78//AC004888

25 F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023 875

F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var1) gene, complete cds.//9.6e-08:730:57//L40608

30 F-MAMMA1002417//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402

35 F-MAMMA1002427//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604

40 F-MAMMA1002428

F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023

45 F-MAMMA1002446//CIT-HSP-2324O22.TR CIT-HSP Homo sapiens genomic clone 2324O22, genomic survey sequence.//2.3e-56:302:95//AQ027479

50 F-MAMMA1002454//Homo sapiens . PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229

55 F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005

F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556

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- 5 F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671
- F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2-  
unordered pieces.//0.025:100:76//AC005077
- 10 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:  
560:98//AF055460
- 15 F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913
- F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-  
10:330:64//AC002477
- 20 F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359
- F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma)  
25 mRNA, complete cds.//1.4e-160:775:97//AF065214
- F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74\_E\_22 complete  
sequence.//1.9e-41:345:80//AC005696
- 30 F-MAMMA1002554
- F-MAMMA1002556
- 35 F-MAMMA1002566
- F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17,  
40 genomic survey sequence.//1.7e-07:76:90//AQ006579
- F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-  
08:195:70//AB018507
- 45 F-MAMMA1002585
- F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete  
50 sequence.//2.1e-26:361:69//AC005019
- F-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548
- 55 F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958

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- F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358.61//AC005220
- 5 F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336.63//AC004861
- 10 F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229.64//AC005486
- F-MAMMA1002618
- 15 F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-71:319:85//AJ010598
- 20 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157.90//AF041449
- F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//8.3e-06:137.72//AE000660
- 25 F-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING DRAFT SEQUENCE.//1.9e-171:819.98//AL031727
- 30 F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478.78//AC003093
- 35 F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499.62//U10063
- F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785.82//AF055666
- 40 F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291.90//AC002038
- 45 F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661.59//L41919
- 50 F-MAMMA1002655//HS\_2003\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198.74//AQ224233
- F-MAMMA1002662
- 55 F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.4e-37:235.84//AC005029

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F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//0.00027:272:64//U22398

5 F-MAMMA1002673

F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3.7e-161:752:99//D86987

10

F-MAMMA1002685//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 394I7, WORKING DRAFT SEQUENCE.//6.2e-45:510:70//AL023585

15

F-MAMMA1002698//HS\_3024\_B1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey sequence.//1.7e-10:155:75//AQ072214

20

F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//5.9e-75:509:83//AF018261

25

F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//1.2e-159:749:99//AB011399

30

F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//3.0e-57:347:79//AL031053

35

F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//3.4e-31:484:69//AC005030

40

F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey sequence.//1.4e-06:265:63//AQ061245

45

F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//0.18:386:58//AL023584

50

F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05:362:63//Z83821

55

F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//0.00010:535:58//AE001368

60

F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.2e-182:880:97//AC005856

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F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055

5 F-MAMMA1002754//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676

10 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902

F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.//5.2e-49:355:81//U73636

15 F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153

20 F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey sequence.//9.7e-21:151:90//AQ028244

25 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//5.6e-105:179:99//U07561

F-MAMMA1002780//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-08, complete sequence.//0.071:277:58//Z98546

30 F-MAMMA1002782//HS\_3213\_B2\_B08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=16 Row=D; genomic survey sequence.//0.00018:219:63//AQ175845

35 F-MAMMA1002796

40 F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; complete sequence.//6.9e-22:332:69//AC002404

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:62//AC003035

45 F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//1.0e-64:320:83//AC002553

50 F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875

F-MAMMA1002835

55 F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462



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F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883

5 F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353

10 F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence.//6.7e-17:383:66//B11616

F-MAMMA1002858

15 F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566

20 F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I25863

F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388

25 F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518

30 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027

35 F-MAMMA1002886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653

40 F-MAMMA1002887//HS\_3238\_B2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814

45 F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906

F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096

50 F-MAMMA1002895//H.sapiens CpG island DNA genomic Mse1 fragment, clone 46b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616

55 F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828

F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:

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457:61//AC002402

5 F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence.//0.25:260:62//AC004467

F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623

10 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193:910:98//AB014598

15 F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//2.7e-23:174:77//AC004032

20 F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome.//1.3e-09:475:61//AF010496

F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5.//0.0029:314:60//AF019366

25 F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//4.0e-10:194:71//Z94056

30 F-MAMMA1002972//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2g10, forward read cpg2g10.ft1aa.//0.38:156:66//Z55272

35 F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//2.9e-41:234:79//AC005919

40 F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//1.7e-05:322:63//AL022098

45 F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence.//0.0064:135:66//AQ275871

50 F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence.//2.8e-31:201:89//B01998

F-MAMMA1003004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031601

55 F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//L04732

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F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139

5 F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//AC003694

10 F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-13:443:61//AC003661

15 F-MAMMA1003019//HS\_3221\_A1\_A01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271

F-MAMMA1003026

20 F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//0.0037:134:73//AC005214

25 F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey sequence.//1.1e-07:66:100//B74936

30 F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.1e-19:220:76//AC004671

35 F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, polymorphic CA repeat, trna and endogenous retrovirus.//9.5e-91:469:78//Z98257

F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//0.21:289:61//AL031321

40 F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//1.7e-139:663:98//AF077952

45 F-MAMMA1003049

50 F-MAMMA1003055//HS\_3014\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940

55 F-MAMMA1003056//HS\_3221\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772

F-MAMMA1003057//M.domesticus MD6 mRNA.//8.5e-128:654:94//X54352

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F-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE.//1.0:142:71//AL034371

5 F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:373:78//AC004796

10 F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166

15 F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:477:64//U72634

F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:85//AF071316

20 F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-58:423:83//X68199

25 F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:676:58//U67916

F-MAMMA1003140

30 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397:97//Y15062

35 F-MAMMA1003150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING DRAFT SEQUENCE.//7.3e-123:266:88//AL021579

F-MAMMA1003166//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//1.6e-33:143:82//Z99716

40 F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//0.50:216:61//Z95400

45 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:92//D31886

F-NT2RM1000032

50 F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds.//6.3e-135:565:84//U67060

F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.1 e-106:542:95//AB014590

55

F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239:60//L27155

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F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-96:535:91//D87671

5 F-NT2RM1000059//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600

10 F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds.//0.54:306:63//U37520

F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:97//AR012692

15 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//1.8e-114:550:97//AB014561

20 F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.63:180:65//AC005594

25 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.027:126:70//AF007155

F-NT2RM1000119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//0.022:644:58//Z97630

30 F-NT2RM1000127//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//1.6e-45:254:94//AQ195884

35 F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds.//5.5e-153:778:95//AB018335

40 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF5 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1e-90:448:97//AF044959

45 F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence.//5.9e-07:66:96//U49890

F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.025:126:70//AF007155

50 F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.1e-05:56:98//AQ261184

55 F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//1.6e-38:711:65//D64009

F-NT2RM1000242

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- 5 F-NT2RM1000244//HS\_2229\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey sequence.//2.0e-  
13:95:95//AQ298474
- 10 F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206\_C\_20, complete  
sequence.//0.023:225:61//AC006070
- F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence.//8.5e-24:  
473:64//Z68336
- 15 F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:455:85//AF035940
- F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e-57:460:  
80//D50920
- 20 F-NT2RM1000271
- F-NT2RM1000272
- 25 F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete  
cds.//6.7e-97:430:92//U11927
- 30 F-NT2RM1000300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097
- 35 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:708:  
92//D63880
- F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds.//5.7e-34:  
182:99//D79205
- 40 F-NT2RM1000341//Homo sapiens full-length insert cDNA clone YP11F06.//1.3e-100:504:  
97//AF085879
- 45 F-NT2RM1000354//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//1.6e-  
11:201:73//AQ218494
- 50 F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:578:  
82//UJ76253
- 55 F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//9.4e-113:367:97//AC004821
- F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:362:

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62//Y08302

5 F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds.//1.0:  
482:58//U26679

F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979

10 F-NT2RM1000399

F-NT2RM1000421//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-  
15 08:195:72//AQ032737

F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete  
20 cds.//3.7e-84:418:97//AF084928

F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:  
69//D79989

25 F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete  
sequence.//4.6e-73:533:83//AC004993

30 F-NT2RM1000553

F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:  
97//AF070542

35 F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000623//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D  
40 Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-  
06:75:89//AQ032737

45 F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribosomal protein  
gene cluster.//1.3e-06:414:61//X15078

F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds.//9.3e-54:  
275:97//AF047695

50 F-NT2RM1000666//HS\_2016\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-  
13:199:73//AQ227865

55 F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3.  
Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and

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another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133

5

F-NT2RM1000672

10

F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348

15

F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627

20

F-NT2RM1000702//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514

25

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832

30

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139

35

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208

F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.92:395:58//AJ011930

40

F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:407:92//L39210

45

F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//AC000380

F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233

50

F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//AC004153

F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207

55

F-NT2RM1000802

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208



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- 5 F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542
- 10 F-NT2RM1000829//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134
- 15 F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.1e-114:683:88//M96629
- 20 F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//AL018762
- 25 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840
- 30 F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378
- 35 F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA143D.//1.2e-31:172:98//K95834
- 40 F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:632:97//AF064605
- 45 F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//AC004228
- 50 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//AF082516
- 55 F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561
- F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280
- F-NT2RM1000898
- F-NT2RM1000905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630
- F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//AC004873

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F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.071:392:60//AC004846

5 F-NT2RM1000962//H.sapiens CpG island DNA genomic MseI fragment, clone 140d1, forward read cpg140d1.ft1a.//4.1e-35:187:99//Z56803

10 F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//AC005959

15 F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//4.0e-160:760:98//U97067

F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//1.7e-11:602:61//U52064

20 F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125

25 F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245

30 F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:261:80//AC005915

F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391

35 F-NT2RM1001072//HS\_3115\_B1\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905

40 F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//AC005263

45 F-NT2RM1001082//Sequence 1 from Patent WO9718303.//2.1e-144:736:95//A62731

F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757

50 F-NT2RM1001092//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489

55 F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964

F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5'UTR).//0.0014:349:61//Z95973

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- 5 F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678
- F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624
- 10 F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755
- 15 F-NT2RM2000006//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291
- 20 F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826
- F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863
- 25 F-NT2RM2000032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379
- 30 F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418
- 35 F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269
- 40 F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905
- F-NT2RM2000101
- 45 F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:97//M12303
- 50 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224
- F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289
- 55 F-NT2RM2000239//F. rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549

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F-nnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292

5 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162

10 F-NT2RM2000259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658

15 F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934

20 F-NT2RM2000287//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656

25 F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864

30 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132

35 F-NT2RM2000363//RPCI11-90B10.TJ RPCI11 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251

40 F-NT2RM2000371//RPCI11-57I4.TJ RPCI11 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343

45 F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514

F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274

50 F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973

55 F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430

F-NT2RM2000420//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D

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Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204

5 F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022

10 F-NT2RM2000452//HS\_3009\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794

15 F-NT2RM2000469//HS\_2019\_A1\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041

20 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290

F-NT2RM2000502

25 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243

F-NT2RM2000522

30

F-NT2RM2000540

35 F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466

40 F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132

40

45 F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252

45

F-NT2RM2000569//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681

50 F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391

55 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987

F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer

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Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466

- 5 F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626
- F-NT2RM2000599//O.sativa osr40g3 gene.//0.30:585:56//Y08988
- 10 F-NT2RM2000609
- F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776
- 15 F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952
- 20 F-NT2RM2000624  
2.9e-06:231:64//Z82061
- F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272
- 25 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558
- 30 F-NT2RM2000639//RPC111-69E5.TJ RPC111 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491
- 35 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576
- F-NT2RM2000669
- 40 F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038
- 45 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984
- F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342
- 50 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244
- F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691
- 55 F-NT2RM2000795//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone

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439F8, WORKING DRAFT SEQUENCE.//1.0e-78:723:76//AL021392

F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228

5

F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//AC005017

10

F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847:99//AB015046

F-NT2RM2000952

15

F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//7.6e-41:239:76//AF109905

20

F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey sequence.//1.1e-11:298:66//AQ035862

25

F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855

30

F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//AF071314

35

F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.3e-145:614:99//AC004873

F-NT2RM2001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//2.7e-95:461:99//AL034380

40

F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-24:726:62//U52064

F-NT2RM2001141

45

F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochochoidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.98:300:62//AL022401

50

F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.2e-147:741:96//AC005488

55

F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete

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cds, UL8 gene, partial cds.//0.026:408:59//U66829

5 F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//2.2e-135:627:98//AC004987

10 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:  
86//AF046700

F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:670:  
55//M26514

15 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150

F-NT2RM2001243

20 F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18,  
genomic survey sequence.//0.0011:274:59//AQ276184

25 F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169

F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15,  
genomic survey sequence.//4.6e-09:156:72//B57734

30 F-NT2RM2001306//RPCI11-28I5.TP RPCI-11 Homo sapiens genomic clone RPCI-11-28I5,  
genomic survey sequence.//0.069:234:64//B84850

35 F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete  
sequence.//1.1e-22:111:81//AC005919

40 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:  
58//AE001118

F-NT2RM2001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
209H1, WORKING DRAFT SEQUENCE.//3.7e-44:340:85//Z84465

45 F-NT2RM2001345//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:  
290:58//AQ089514

50 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-  
screen.//5.0e-60:365:87//U56429

55 F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete  
sequence.//0.98:415:58//AC004899

F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT



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Region, complete sequence.//4.0e-54:394:75//AC004033

5 F-NT2RM2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520

10 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:  
99//AJ007509

F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete  
cgs.//7.1e-91:601:83//AB000113

15 F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete  
sequence.//0.81:200:69//AC005624

20 F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment  
No. 2.//3.8e-16:316:65//Z99708

F-NT2RM2001544

25 F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:  
318:67//AL032657

30 F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:  
582:64//M34551

F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750

35 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902

40 F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:  
90//AF032667

F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell  
leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431

45 F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:  
85//M96630

50 F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete  
sequence.//1.5e-50:561:71//AC004691

55 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:  
98//AB014518

F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey  
sequence.//2.5e-13:224:64//Z91020

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- 5 F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913
- F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629
- 10 F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.2e-153:807:93//AF023451
- 15 F-NT2RM2001659//nxb0002cE07f CUGI Rice BAC Library Oryza sativa genomic clone nxb0002J13f, genomic survey sequence.//1.0:485:56//AQ051653
- 20 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//3.7e-172:802:99//AF044195
- F-NT2RM2001668
- 25 F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2e-18:279:70//AJ003147
- 30 F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA; complete cds.//1.6e-137:683:94//U21157
- 35 F-NT2RM2001675//RPC11-51J16.TJ RPC11 Homo sapiens genomic clone R-51J16, genomic survey sequence.//1.0:394:58//AQ053677
- F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAll project).//0.87:220:61//AL021890
- 40 F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948
- 45 F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey sequence.//3.2e-53:241:82//B59854
- 50 F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2.//1.2e-05:306:58//M10668
- 55 F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920
- F-NT2RM2001699//HS\_3195\_8B2\_DO1\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-

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07:322:61//AQ189056

5 F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//Z95556

10 F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469

F-NT2RM2001716

15 F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290

20 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-111:530:98//AB007931

25 F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//3.1e-102:248:95//AJ010598

F-NT2RM2001743

30 F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.11:138:66//Z68117

35 F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds.//9.4e100:418:88//M96629

40 F-NT2RM2001768//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993

45 F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.3e-66:680:72//AC006116

F-NT2RM2001782

50 F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053

F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770

55

F-NT2RM2001797//HS\_3045\_AT\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey sequence.//1.4e-

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74:381:97//AQ129456

F-NT2RM2001800

5

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195

10

F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126

15

F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//3.3e-16:109:95//B89870

20

F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759

25

F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//AC002347

30

F-NT2RM2001855//HS\_3224\_A1\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=O, genomic survey sequence.//0.00012:68:91//AQ205285

35

F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSSs, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177

45

F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610

50

F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence.//8.6e-30:613:63//X59720

55

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931

F-NT2RM2001930//M.musculus mRNA for semaphorin G.//4.7e-117:730:85//X97818

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- F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028
- 5 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080
- 10 F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700
- 15 F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.//0.42:179:65//AC005825
- 20 F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//AF089816
- F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981
- 25 F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:95//D16955
- F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151
- 30 F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407
- 35 F-NT2RM2002014
- F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransferase mRNA, complete cds.//1.5e-89:822:74//U00932
- 40 F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132
- F-NT2RM2002055
- 45 F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//AF073936
- 50 F-NT2RM2002091//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380
- 55 F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840
- F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1)

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mRNA, complete cds.//2.4e-143:684:98//AF030435

5 F-NT2RM2002128//*Mesocricetus auratus* guanine nucleotide-binding protein beta 5 (Gnb5)  
mRNA, complete cds.//7.0e-27:330:73//U13152

10 F-NT2RM2002142//*Danio rerio* gastrulation specific (G12) mRNA, complete cds.//6.3e-10:  
135:80//U27121

F-NT2RM2002145//*Homo sapiens* erythroblast macrophage protein EMP mRNA, complete  
cds.//4.2e-143:800:92//AF084928

15 F-NT2RM2002178//*Homo sapiens* mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:  
97//AB007936

20 F-NT2RM2002580//*Drosophila melanogaster* DNA sequence (P1 DS02110 (D147)),  
complete sequence.//7.4e-13:337:62//AC004423

F-NT2RM4000024//*D.melanogaster* DmRP128 gene for RNA polymerase III second-largest  
subunit.//1.2e-62:801:70//X58826

25 F-NT2RM4000027//*Caenorhabditis elegans* cosmid F09E5.//0.36:336:60//U37429

30 F-NT2RM4000030//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 56h10,  
forward read cpg56h10.ft1a.//9.3e-22:127:100//Z55685

F-NT2RM4000046//*Curcubita maxima* 25S - 18S rDNA intergenic spacer.//4.1e-05:386:  
60//X13059

35 F-NT2RM4000061

40 F-NT2RM4000085//*B.taurus* mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829

F-NT2RM4000086

45 F-NT2RM4000104//*Homo sapiens* chromosome 16 zinc finger protein ZNF210 (ZNF210)  
mRNA, complete cds.//4.2e-23:345:69//AF060865

F-NT2RM4000139//*R.norvegicus* trg mRNA.//1.4e-56:708:69//X68101

50 F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP *Homo sapiens* genomic clone 2282N15,  
genomic survey sequence.//3.0e-09:88:90//AQ000070

55 F-NT2RM4000156//*H.sapiens* HPBR11-7 gene.//2.0e-21:586:60//X67336

F-NT2RM4000167//*Mouse* kif4 mRNA for microtubule-based motor protein KIF4, complete  
cds.//2.7e-143:810:90//D12646

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- 5 F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157
- F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:60//AF051726
- 10 F-NT2RM4000197
- F-NT2RM4000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//0.67:461:60//AL031667
- 15 F-NT2RM4000200
- F-NT2RM4000202//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34c2, forward read cpg34c2.ft1a.//1.7e-27:190:90//Z65361
- 20 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255
- 25 F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:62//J03852
- 30 F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//4.6e-102:233:94//AC005383
- 35 F-NT2RM4000233//Mus musculus semaphorin VIa mRNA, complete cds.//1.6e-135:835:86//AF030430
- F-NT2RM4000244//RPCI11-24P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P15, genomic survey sequence.//5.5e-08:422:62//B86757
- 40 F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//0.98:207:60//AC005855
- 45 F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing human mRNA for T-cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689
- 50 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//M99438
- F-NT2RM4000324
- 55 F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085

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F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430

5 F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700

10 F-NT2RM4000354//HS\_2221\_A2\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449

15 F-NT2RM4000356

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//1.6e-133:628:99//AB014542

20 F-NT2RM4000368//RPCI11-91B5.TJ RPCI11 Homo sapiens genomic clone R-91B5, genomic survey sequence.//5.0e-12:431:61//AQ283217

25 F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds.//7.4e-86:845:72//AF059485

30 F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965.//2.5e-34:767:61//D44597

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.5e-15:114:94//AB015046

35 F-NT2RM4000421

F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//1.5e-37:295:82//AC005921

40

F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//3.9e-94:740:78//AF062476

45 F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence.//1.5e-22:149:92//AQ062111

50 F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//1.3e-76:386:97//AJ010952

55 F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, //1.1e-22:356:67//AB000459

F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.53:198:70//AC005908



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F-NT2RM4000511

5 F-NT2RM4000514

F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 2285L3,  
genomic survey sequence.//0.0012:200:66//AQ000113

10 F-NT2RM4000520

F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//2.9e-31:732:  
64//M58297

15 F-NT2RM4000532//HS\_3231\_B1\_C05\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-  
59:362:90//AQ192093

20 F-NT2RM4000534

F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18,  
genomic survey sequence.//1.1e-34:208:93//AQ260706

25 F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14,  
genomic survey sequence.//8.3e-34:180:99//AQ004125

30 F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete  
sequence.//1.2e-09:203:66//AC005288

35 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:  
68//AB002390

40 F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21,  
genomic survey sequence.//8.4e-16:109:94//B89870

45 F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:  
68//Z46786

F-NT2RM4000674

50 F-NT2RM4000689//CIT-HSP-2381O13.TF CIT-HSP Homo sapiens genomic clone 2381O13,  
genomic survey sequence.//2.6e-31:174:97//AQ110303

F-NT2RM4000698

55 F-NT2RM4000700

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F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789

5 F-NT2RM4000717

F-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379

10

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303

15

F-NT2RM4000741

F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593

20

F-NT2RM4000764

F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790

25

F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920

30

F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCFS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206

35

F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//AC005306

40

F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds.//5.9e-97:857:74//U41663

45

F-NT2RM4000796//HS\_3214\_B1\_F11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988

50

F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//6.2e-78:816:72//AF023451

55

F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109

F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406

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F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373

5 F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.0:477:56//AC005940

F-NT2RM4000852

10

F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence.//3.4e-29:229:83//AC003957

15 F-NT2RM4000887

F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004

20

F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929

25 F-NT2RM4000971//RPCI11-53H3.TJ RPCI11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735

30 F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.3e-19:207:78//AC005245

F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651

35

F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272

40 F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539

45 F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276

F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858

50 F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629

55 F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479

F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid

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Homosapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776

5 F-NT2RM4001116

F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593

10 F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-PRF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249

15 F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706

20 F-NT2RM4001160

F-NT2RM4001187

25 F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378

F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:799:69//X78933

30 F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//4.2e-152:707:99//AF004828

35 F-NT2RM4001204

F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:70//AF005381

40 F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884

45 F-NT2RM4001258//HS\_3171\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676

50 F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163

55 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973

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F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002

5 F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016

10 F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127

15 F-NT2RM4001344//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388

F-NT2RM4001347

20 F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786

25 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799

30 F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393

F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023

35 F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526

40 F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183

45 F-NT2RM4001414//Homo sapiens full-length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563

F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226

50 F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901

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F-NT2RM4001454

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- F-NT2RM4001455
- 5 F-NT2RM4001483//Human zinc finger protein ZNF136.//3.2e-36:329:78//J09367
- F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585
- 10 F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688
- 15 F-NT2RM4001522//Human HepG2 3' region Mbol cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274
- F-NT2RM4001557
- 20 F-NT2RM4001565
- F-NT2RM4001566
- 25 F-NT2RM4001569//HS\_2050\_B1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720
- 30 F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//AF071317
- 35 F-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942
- F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces.//0.34:388:59//AC002355
- 40 F-NT2RM4001597//M.musculus red-1 gene.//6.2e-139:788:90//X92750
- F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334
- 45 F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592.//2.5e-05:490:58//D90910
- 50 F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//J38196
- 55 F-NT2RM4001650//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0435P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

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F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320

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F-NT2RM4001666

F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence.//3.2e-35:240:87//AF046699

10

F-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//1.9e-151:564:97//AL031447

15

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957

F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.2e-91:488:94//AL034430

20

F-NT2RM4001731//Orang-utan in volucrin gene, complete cds.//0.40:530:59//M25312

25

F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123

F-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING DRAFT SEQUENCE.//2.3e-49:320:89//AL031709

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F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//6.3e-64:379:76//AC005831

35

F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868

40

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270

F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017

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F-NT2RM4001810

F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//7.1e-31:176:84//AC005036

50

F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//4.4e-34:195:95//M37712

55

F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.3e-51:490:75//U49046

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- 5 F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:72//J28687
- F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//1.0:406:60//AC000076
- 10 F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2, complete cds.//1.6e-131:831:86//AF033275
- 15 F-NT2RM4001842//HS\_3163\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513
- 20 F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855
- F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//J64433
- 25 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6.9e-149:704:98//Y17711
- 30 F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.//5.7e-48:600:68//Z88651
- F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey sequence.//0.0025:61:88//AQ060809
- 35 F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335
- 40 F-NT2RM4001922//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732
- 45 F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence.//4.9e-10:269:63//AB005248
- 50 F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//7.6e-152:311:100//AC005207
- F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162
- 55 F-NT2RM4001953//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046



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- 5 F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868
- F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330
- 10 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341
- 15 F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:502:60//Z82253
- 20 F-NT2RM4001987//RPC11-49L11.TJ RPC11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//2.6e-33:177:99//AQ051701
- F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//0.019:65:90//AC005921
- 25 F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:57//L15344
- 30 F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712
- 35 F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//U01882
- 40 F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473:76//AC005283
- F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540
- 45 F-NT2RM4002062//Drosophila melanogaster, Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122
- 50 F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//U82267
- 55 F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783
- F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//1.1e-53:295:76//AC005216

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- 5 F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:  
277:75//AF072758
- 10 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete  
cds.//9.0e-23:588:61//AF059569
- 15 F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:  
69//X60789
- 20 F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete  
cds.//2.0e-121:762:86//D12646
- 25 F-NT2RM4002128//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-  
18:117:95//AQ186312
- 30 F-NT2RM4002140
- 35 F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete  
sequence.//1.8e-49:736:65//AC004152
- 40 F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940
- 45 F-NT2RM4002161//Homo sapiens mRNA for LAFPTPase, isoform 1, partial.//4.2e-151:763:  
96//AJ130763
- 50 F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete  
genome.//2.1e-16:580:60//AE000540
- 55 F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome  
22q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636
- F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//3.2e-132:782:  
87//AF030430
- F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G  
mRNA, complete cds.//1.5e-40:292: 84//L14684
- F-NT2RM4002213
- F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160
- F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete  
sequence.//1.0:428:58//AC004448

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F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959

5 F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006118aG12, genomic survey sequence.//3.3e-12:217:67//AL024779

10 F-NT2RM4002278//HS\_3089\_A1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=1, genomic survey sequence.//1.9e-64:381:92//AQ121653

15 F-NT2RM4002281  
F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515

20 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457

25 F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881

30 F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822

35 F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865

F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849

40 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549

45 F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC002978

50 F-NT2RM4002383//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284

F-NT2RM4002390

55 F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110

F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-

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16:468:59//AE001092

5 F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336

10 F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845

F-NT2RM4002452

15 F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988

20 F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690

25 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255

F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591

30

F-NT2RM4002493

35 F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484

40 F-NT2RM4002504//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//3.8e-31:233:87//AL031577

F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162

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F-NT2RM4002532

F-NT2RM4002534

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F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759

55

F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//AF022962

F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7,

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genomic survey sequence.//8.5e-31:220:88//AQ263402

- 5 F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344
- 10 F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875
- 15 F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454
- 20 F-NT2RM4002623//Drosophila melanogaster, Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122
- 25 F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385
- 30 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449
- 35 F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047
- 40 F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784
- 45 F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//2.8e-183:548:91//X98834
- 50 F-NT2RP1000101//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward read cpg28b4.ft1a.//6.0e-27:163:95//Z60555
- 55 F-NT2RP1000111//CIT-HSP-2307O14.TR CIT-HSP Homo sapiens genomic clone 2307O14, genomic survey sequence.//1.2e-11:128:81//AQ016069
- F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//M86699
- F-NT2RP1000124//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557
- F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:681//E08546
- F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792
- F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1

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unordered pieces.//1.9e-20:431:64//AC006030

5 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence.//2.5e-138:679:97//AF070535

F-NT2RP1000191

10 F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220:61//D89496

15 F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//4.7e-51:508:69//AC004373

F-NT2RP1000259

20 F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds.//7.8e-142:866:88//AF042383

25 F-NT2RP1000324//RPC111-81O21.TJ RPC111 Homo sapiens genomic clone R-81O21, genomic survey sequence.//2.8e-29:182:92//AQ285136

30 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//4.2e-147:693:98//AF053551

F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence.//1.4e-08:281:61//Z75525

35 F-NT2RP1000348//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c.//1.7e-09:71:100//Z56610

F-NT2RP1000357

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F-NT2RP1000358 5.7e-16:403:61//AC005456

45 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538

50 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds.//1.8e-176:877:96//AF064594

F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558

55 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9.4e-178:710:98//AB011159

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F-NT2RP1000416

5 F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of  
cds.//1.0:198:60//L40178

10 F-NT2RP1000439//HS\_2182\_A1\_D06\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence.//2.1e-  
68:441:87//AQ024305

15 F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28,  
WORKING DRAFT SEQUENCE.//3.8e-57:185:88//AP000047

F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete  
sequence.//2.7e-132:204:99//AC004453

20 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic  
sequence, complete sequence.//4.9e-80:196:95//AC002985

25 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds.//1.9e-  
55:440:80//U47634

30 F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome  
1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuroneurin, Myotendinous  
antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene  
preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//2.6e-92:  
562:88//Z99297

35 F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2.0e-130:622:  
98//D87686

40 F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes,  
complete cds's.//0.11:360:58//M81648

45 F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8  
unordered pieces.//4.9e-34:209:93//AC004895

F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein CHOp24  
mRNA, partial cds.//1.2e-08:331:63//U26264

50 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial  
cds.//4.4e-81:295:92//AF017418

55 F-NT2RP1000577//HS\_2228\_B2\_C05\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-  
31:179:75//AQ185128

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F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620

5 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770

10 F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419

15 F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989

F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943

20 F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form) .//5.2e-10:120:80//X69907

25 F-NT2RP1000695

F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//I30536

30 F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-19:188:81//AC004932

F-NT2RP1000730

35 F-NT2RP1000733//Human chromosome 16p13-1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742

40 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//8.0e-122:604:96//AF101434

45 F-NT2RP1000746//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//1.5e-83:466:92//AQ186344

50 F-NT2RP1000767//Homo sapiens full-length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442

F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

55 F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213



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- 5 F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244
- 10 F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837
- F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020
- 15 F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398
- 20 F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629
- 25 F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812
- 30 F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840
- 35 F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094
- F-NT2RP1000902//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199
- 40 F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761
- 45 F-NT2RP1000916
- F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:72//L49362
- 50 F-NT2RP1000944//HS\_2179\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269
- 55 F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483
- F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo

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sapiens genomic clone cSRL-143G4, genomic survey sequence.//0.030:89:78//B01950

5 F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence.//3.9e-11:  
445:61//Z49068

F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.3e-  
57:326:92//AC004263

10 F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:981/M60858

15 F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10,  
genomic survey sequence.//0.32:137:68//AQ017126

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435

20 F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene, complete  
cds, and TH1 gene, partial cds.//1.3e-31:497:65//U34925

25 F-NT2RP1001013//HS\_3068\_B1\_809\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-  
24:414:66//AQ127667

30 F-NT2RP1001014//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey  
sequence.//0.00052:83:81//AQ304711

35 F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC-1073\_F\_15, complete  
sequence.//1.3e-134:241:99//AC004686

40 F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete  
sequence.//2.5e-59:451:83//AC004993

F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete  
cds.//4.5e-93:476:96//U82267

45 F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18  
unordered pieces.//6.6e-54:217:89//AC004938

50 F-NT2RP1001113

F-NT2RP1001173

55 F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:  
373:681/U79139

F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3

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unordered pieces.//3.5e-32:388:73//AC006039

F-NT2RP1001199

5

F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508

10

F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128 :99//AC002036

15

F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4-3e-91:344:93//AF029914

20

F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's-//0.54:292:63//L44140

F-NT2RP1001294

F-NT2RP1001302

25

F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750

30

F-NT2RP1001311//RPCI11-67O14.TK RPCI11 Homo sapiens genomic clone R-67O14, genomic survey sequence.//0.26:80:75//AQ239291

35

F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228

40

F-NT2RP1001361//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647

F-NT2RP1001385

45

F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316

50

F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257120 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878

55

F-NT2RP1001424

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F-NT2RP1001432

5 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149

10 F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737

15 F-NT2RP1001466//HS\_3006\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336

F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375

20 F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.1/4-0e-87:563:85//L11316

F-NT2RP1001494

25 F-NT2RP10015431/Drosophila melanogaster DNA sequence (P1 DS01142 (D148)), complete sequence.//1.9e-27:387:67//AC004280

30 F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840

35 F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343

F-NT2RP100T616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913

40 F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence.//2.4e-45:305:88//B69912

45 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081

50 F-NT2RP2000006//HS\_3061\_B2\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:68//AB002390

55 F-NT2RP2000008//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424

F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete

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sequence.//1.4e-32:345:75//AC005066

5 F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey  
sequence.//5.0e-41:445:72//Z88655

10 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:  
97//AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1)  
mRNA, complete cds.//2.4e-95:467:97//AF061749

15 F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24,  
genomic survey sequence.//3.3e-39:236:91//AQ043092

20 F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-  
50:311:90//D78610

25 F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:  
66//AF059485

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete  
sequence.//2.0e-118:597:95//AC005754

30 F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:  
60//AC006037

35 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete  
cds.//2.1e-77:278:97//AF050079

40 F-NT2RP2000079//H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward  
read cpg40c2.ft1k.//3.2e-33:197:95//Z55440

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:  
98//AB018338

45 F-NT2RP2000091//HS\_2228\_A2\_B02\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:  
55:90//AQ146363

50 F-NT2RP2000097

55 F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2  
unordered pieces.//2.5e-05:482:60//AC004961

F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete  
sequence.//1.0e-22:274:69//AC003973

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- 5 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356
- 10 F-NT2RP2000120//HS\_3000\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365
- 15 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177
- 20 F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827
- 25 F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419
- 30 F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.45:377:58//AL034370
- 35 F-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924
- 40 F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431
- 45 F-NT2RP2000173
- 50 F-NT2RP2000175
- 55 F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295
- F-NT2RP2000195//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581
- F-NT2RP2000205
- F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence.//7.2e-80:170:90//AC003030
- F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-64:400:85//AC004382

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- 5 F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs.//2.2e-07:280:66//Z97632
- 10 F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//8.8e-30:508:67//U88401
- 15 F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:87//AC004066
- F-NT2RP2000248
- 20 F-NT2RP2000257//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0078:286:60//AL021388
- 25 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey sequence.//5.7e-82:416:97//AQ059184
- F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//4.5e-29:310:73//AC006116
- 30 F-NT2RP2000274
- F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6.3e-20:260:73//X74904
- 35 F-NT2RP2000288
- 40 F-NT2RP2000289
- F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//4.6e-69:744:70//M27877
- 45 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL021530
- F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173:76//AC006082
- 50 F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.3e-144:731:95//AL022398
- 55

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F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12  
Contains ESTs and GSSs, complete sequence.//1.9e-102:555:90//AL034430

5 F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete  
cds.//6.4e-105:639:87//M25757

10 F-NT2RP2000337//HS\_2060\_B1\_E01\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey sequence.//0.78:  
218:60//AQ243333

15 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete  
cds.//3.6e-129:627:97//U83981

20 F-NT2RP2000369//HS\_2182\_B1\_B11\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-  
87:421:99//AQ024835

25 F-NT2RP2000412//Human DNA sequence from PAC 124O9 on chromosome 6q21.  
Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.72:170:65//AL021327

F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-66:375:  
93//L28010

30 F-NT2RP2000420//Homo sapiens full-length insert cDNA YQ86E07.//9.2e-77:423:  
93//AF075093

35 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,  
complete cds.//2.1e-126:609:96//AF102265

40 F-NT2RP2000438//CITBI-E1-2519O19.TR CITBI-E1 Homo sapiens genomic clone 2519O19,  
genomic survey sequence.//0.96:61:78//AQ276878

F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete  
sequence.//7.1e-17:341:67//AC004691

45 F-NT2RP2000459//H.sapiens mRNA for imogen 38.//5.7e-21:158:87//Z68747

50 F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains  
ESTs.//3.2e-11:160:73//Z92844

F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete  
sequence.//0.0031:187:66//AC005229

55 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey  
sequence.//8.8e-07:179:64//AL026277



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F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence.//0.19:72:81//U21671

5 F-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//5.0e-115:570:96//AL022318

10 F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//8.4e-37:196:98//AB005543

15 F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//AC005321

F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514

20 F-NT2RP2000644//HS\_3211\_A1\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486

25 F-NT2RP2000656

F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386

30 F-NT2RP2000668

35 F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916

40 F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913

45 F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122

F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540

50 F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965

55 F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293

F-NT2RP2000764//HS\_2254\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D

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Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45:95//AQ068887

5 F-NT2RP2000809

F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698

10 F-NT2RP2000814

F-NT2RP2000816

15 F-NT2RP2000819

F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292

20

F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479

25 F-NT2RP2000845

F-NT2RP2000863//Human partial cDNA sequence, clone x874.//5.9e-29:173:94//Z47045

30 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284

F-NT2RP2000892

35

F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3.4e-129:610:98//AB018266

40 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014

45 F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890

50 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298

F-NT2RP2000965

55 F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393

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- 5 F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//1.6e-72:498:82//AC005277
- F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394
- 10 F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167
- 15 F-NT2RP2001044//HS\_2253\_B1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224
- 20 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957
- F-NT2RP2001065
- 25 F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561
- 30 F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423
- F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063
- 35 F-NT2RP2001119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596
- 40 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072
- 45 F-NT2RP2001137//HS\_2193\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187
- 50 F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076
- 55 F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a

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putative CpG island, complete sequence.//0.23:207:66//AL009178

- 5 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949
- 10 F-NT2RP2001174//RPC111-58L2.TK RPC111 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306
- F-NT2RP2001196
- 15 F-NT2RP2001218
- F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893
- 20 F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760
- F-NT2RP2001245//HS\_3062\_B1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177
- 25 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353
- 30 F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430
- 35 F-NT2RP2001290//M.musculus mRNA for I47 clone.//8.6e-102:641:86//X61455
- F-NT2RP2001295//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594
- 40 F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M22967
- F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M80783
- 45 F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence.//1.3e-65:366:94//AQ038539
- 50 F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147
- 55 F-NT2RP2001366//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4e11, forward read cpg4e11.f1a.//1.7e-12:98:92//Z61305
- F-NT2RP2001378//HS\_3054\_B2\_A03\_MR CIT Approved Human Genomic Sperm Library D

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Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence.//9.8e-17:131:89//AQ100721

- 5 F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371
- F-NT2RP2001392//S.pristinaespiralis snbC gene & amp; snbDE gene.//0.019:267:59//Y11548
- 10 F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242
- 15 F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219
- F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759
- 20 F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//AF015454
- 25 F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065
- F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702
- 30 F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350
- 35 F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275
- F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931
- 40 F-NT2RP2001450
- 45 F-NT2RP2001467
- F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561
- 50 F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-22:462:64//AF005355
- 55 F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.0e-136:657:97//Y14494

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- F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-37:357:64//AC004596
- 5 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586
- F-NT2RP2001560
- 10 F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//4.4e-123:590:98//AB007957
- 15 F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:580:58//U32943
- F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds.//6.5e-09:222:66//AF030430
- 20 F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648
- 25 F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340
- 30 F-NT2RP2001613
- F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp.//1.7e-15:279:68//Z36784
- 35 F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//5.4e-123:606:96//AF030233
- F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//4.2e-144:687:97//AF058718
- 40 F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase.//1.0e-36:372:74//X84907
- 45 F-NT2RP2001675//S.pombe chromosome I cosmid c2G11.//0.070:507:59//Z54354
- F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259
- 50 F-NT2RP2001678//HS\_2007\_A2\_A04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699
- 55 F-NT2RP2001699//RPCI11-57B17.TK RPCI11 Homo sapiens genomic clone R-57B17,

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genomic survey sequence.//0.99:141:63//AQ115592

5 F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete  
sequence.//9.4e-117:604:95//AC004079

10 F-NT2RP2001721//Homo sapiens DNA sequence from clone 466I8 on chromosome Xq11.1-  
13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C  
Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC  
1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//1.0:273:  
61//AL030998

15 F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR  
Region, complete sequence.//1.0:356:62//AC000090

20 F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:  
86//D14697

25 F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482),  
complete sequence.//6.0e-145:715:97//AC004783

F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete  
sequence.//0.38:340:60//AE001378

30 F-NT2RP2001839//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D\_  
Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:  
253:60//AQ090347

35 F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610

40 F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:  
62//AF027219

F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete  
cds.//2.8e-44:483:71//AB012309

45 F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3  
Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2  
(DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.8e-87:496:92//AL031864

50 F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3'  
end.//9.2e-112:633:90//M74161

55 F-NT2RP2001900//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281

F-NT2RP2001907//H.sapiens CpG island DNA genomic MseI fragment, clone 97f11,

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forward read cpg97f11.ft1a.//4.2e-26:206:84//Z64125

- 5 F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688
- 10 F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856
- F-NT2RP2001943//Drosophila melanogaster cosmid 25E8.//0.00036:248:60//AL009196
- 15 F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-78:232:99//AC005033
- 20 F-NT2RP2001947//Homo sapiens full-length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442
- F-NT2RP2001969//H.sapiens CpG island DNA genomic Mse1 fragment, clone 152a8, reverse read cpg152a8.rt1a.//1.0e-20:123:99//Z59378
- 25 F-NT2RP2001976
- F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117
- 30 F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022
- 35 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299
- 40 F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//0.76:189:65//AC005895
- 45 F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-12:160:79//AC004825
- F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029
- 50 F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//2.2e-86:722:77//AC004552
- 55 F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375



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F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301

5 F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//U87306

10 F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein {alternatively spliced, exon 10 to 13 region} [human, Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083

15 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183

20 F-NT2RP2002078//F12O16-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//0.14:191:64//AQ249805

F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917

25 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509

30 F-NT2RP2002105//H.sapiens CpG island DNA genomic Mse1 fragment, clone 10h8, forward read cpg10h8.ft1a.//2.4e-29:178:94//Z58857

35 F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey sequence.//2.5e-32:202:92//B64468

F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//M25874

40 F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923

45 F-NT2RP2002172//HS\_3020\_B1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169

50 F-NT2RP2002185//RPC11-67B15.TJ RPC11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//2.8e-18:109:100//AQ201833

F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl1) mRNA, complete cds.//2.7e-36:363:78//U09215

55 F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-82:477:89//AF032872

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F-NT2RP2002208

5 F-NT2RP2002219//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//1.0:378:58//AL034557

10 F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308

15 F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998

F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//J22394

20 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418

25 F-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//9.7e-67:340:89//AL033527

30 F-NT2RP2002270//RPC111-77C23.TV RPC111 Homo sapiens genomic clone R-77C23, genomic survey sequence.//2.9e-18:79:93//AQ268098

F-NT2RP2002292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//1.0:290:60//AL031033

35 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//AF069532

40 F-NT2RP2002316//HS\_2171\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673

45 F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//3.9e-123:640:95//AB015594

F-NT2RP2002333

50 F-NT2RP2002373//F.rubripes GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//Z87330

55 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958

F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:

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56//X95275

- 5 F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey sequence.//5.7e-15:220:71//AL015615
- F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9.//7.1e-71:582:80//AJ223742
- 10 F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF016682
- F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U88169
- 15 F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//1.9e-06:281:66//AC004381
- F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:63//D42045
- 20 F-NT2RP2002475
- F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//2.4e-123:607:96//AB005289
- 25 F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF069300
- 30 F-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//7.2e-18:134:90//AC006213
- F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-157:761:97//AB018334
- 35 F-NT2RP2002520
- 40 F-NT2RP2002537
- F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127
- 45 F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC005317
- 50 F-NT2RP2002591//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304
- F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR012155
- 55 F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9e-43:282:87//U19181

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- 5 F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF051310
- 10 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp.//5.6e-27:460:63//Y10806
- 15 F-NT2RP2002621
- 20 F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1.//0.023:322:60//D90397
- 25 F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384
- 30 F-NT2RP2002701//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380
- 35 F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980
- 40 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.5e-40:631:65//AB014572
- 45 F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:600:73//AF041107
- 50 F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL033388
- 55 F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface protein (PSSP15) gene, complete cds; ORF, 5' end.//0.0073:274:66//M94861
- F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D89016
- F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296
- F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence.//1.7e-08:206:63//AC002433
- F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171
- F-NT2RP2002769//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//J78289

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F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5,  
genomic survey sequence.//6.8e-18:186:79//B69837

5 F-NT2RP2002800

F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing  
uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-41:134:  
10 94//AC006078

F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA,  
partial cds, clone TRB-4.//0.85:93:68//M18845

15 F-NT2RP2002862//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//5.0e-  
67:390:91//AQ186344

20 F-NT2RP2002880

F-NT2RP2002891//CIT-HSP-2310O14.TF CIT-HSP Homo sapiens genomic clone 2310O14,  
25 genomic survey sequence.//0.11:53:90//AQ019792

F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511

30 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete  
cds.//2.3e-135:628:99//AF038392

F-NT2RP2002929//F.rubripes GSS sequence, clone 123I23aA1, genomic survey  
35 sequence.//3.9e-06:66:83//AL017246

F-NT2RP2002939

40 F-NT2RP2002954

F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete  
cds.//1.3e-47:411:79//U62483

45 F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 2340D12,  
genomic survey sequence.//4.6e-96:476:97//AQ057233

50 F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-  
09:272:61//AF059569

55 F-NT2RP2002987//Homo sapiens (subclone 6\_d9 from P1 H21) DNA sequence, complete  
sequence.//1.0e-22:293:67//AC000958

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- 5 F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424
- F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765
- 10 F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//4.2e-23:202:82//AC005703
- 15 F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822
- 20 F-NT2RP2003099//HS\_3008\_B2\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786
- F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362
- 25 F-NT2RP2003117//HS\_2034\_B2\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797
- 30 F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765
- 35 F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329
- F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915
- 40 F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976
- 45 F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716
- 50 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025
- F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657
- 55 F-NT2RP2003164
- F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein

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gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43 :334:79//U91328

5 F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040

10 F-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597

F-NT2RP2003206

15 F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794

F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:86//AF023657

20 F-NT2RP2003237//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447

25 F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107

30 F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481

F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833

35 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525

40 F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286

45 F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024

F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973

50 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572

55 F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722

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- F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666
- 5 F-NT2RP2003308//D.melanogaster crn mRNA.//1.1e-63:697:70//X58374
- F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//0.040:145:64//AC005288
- 10 F-NT2RP2003339
- F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559
- 15 F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510
- 20 F-NT2RP2003391
- F-NT2RP2003393//HS\_3218\_A2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356
- 25 F-NT2RP2003394
- 30 F-NT2RP2003401
- F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630
- 35 F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023
- 40 F-NT2RP2003446
- F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.0018:366:60//AJ235272
- 45 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//7.5e-16:189:68//AC004770
- 50 F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977
- 55 F-NT2RP2003499 2.1e-08:408:61//AB000826
- F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12



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unordered pieces.//1.9e-33:192:96//AC005236

5 F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds.//1.0:328:60//AB013801

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:93//D87460

10 F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X03702

15 F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.3e-101:564:91//M21977

20 F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2.0e-40:315:75//Z80899

F-NT2RP2003543

25 F-NT2RP2003559//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a.//1.1e-20:122:99//Z56144

30 F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//8.8e-27:664:63//M34551

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds.//4.1e-113:541:98//AB007931

35 F-NT2RP2003581

40 F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic survey sequence.//J1.9e-11:210:65//AL012756

F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//1.9e-123:587:98//AF030233

45 F-NT2RP2003629

50 F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//7.8e-88:582:84//AJ006215

F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//5.6e-47:335:83//AC005081

55 F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//1.2e-06:133:74//AC003684

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F-NT2RP2003691//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL023807

5 F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds.//1.3e-65:458:82//U44803

10 F-NT2RP2003704//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2a9, reverse read cpg2a9.rt1e.//3.8e-17:170:84//Z60615

15 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-108:518:98//AB011097

20 F-NT2RP2003713//HS\_2016\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895

F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//AC003973

25 F-NT2RP2003727//RPCI11-77I19.TV RPCI11 Homo sapiens genomic clone R-77I19, genomic survey sequence.//3.4e-26:294:74//AQ268303

30 F-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-74:194:91//AC004951

35 F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-92:165:96//AC003964

F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987

40 F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence.//1.0:109:69//AB013275

45 F-NT2RP2003769

F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//3.0e-96:467:98//AC004771

50 F-NT2RP2003777

55 F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//7.2e-107:731:82//S70011

F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761

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- F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//8.9e-06:151:74//AC004491
- 5 F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.//0.018:145:69//AC005167
- 10 F-NT2RP2003857//HS\_3227\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey sequence.//0.96:257:61//AQ303467
- 15 F-NT2RP2003859
- F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC002375
- 20 F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence.//0.13:167:64//AQ265722
- 25 F-NT2RP2003912//nek1=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:838:86//S45828
- F-NT2RP2003952
- 30 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014458
- 35 F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase
- 40 Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1).
- 45 Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL031282
- F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347
- 50 F-NT2RP2003984
- 55 F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382

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F-NT2RP2003988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681

5 F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:91//AL023580

10 F-NT2RP2004014

F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427:87//AC004780

15 F-NT2RP2004042

F-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134O19, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555

20 F-NT2RP2004081

25 F-NT2RP2004098//HS\_2216\_A1\_B12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694

30 F-NT2RP2004124//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993

35 F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220:62//AB007645

40 F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493

F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140

45 F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162:66//AF028235

50 F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL021816

F-NT2RP2004187//Homo sapiens full-length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093

55 F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998

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F-NT2RP2004196

5 F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386:61//M60676

10 F-NT2RP2004226//HS\_2186\_A1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813

F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448:67//X75756

15 F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718

20 F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006

F-NT2RP2004242

25 F-NT2RP2004245

F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL034446

30 F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781

35 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416

40 F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267:59//AC004423

F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519

45 F-NT2RP2004347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650

50 F-NT2RP2004364

F-NT2RP2004365

55 F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864

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- F-NT2RP2004373//Homo sapiens cosmids Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397
- 5 F-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969
- 10 F-NT2RP2004392
- F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164
- 15 F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799
- F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441
- 20 F-NT2RP2004412//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34g4, reverse read cpg34g4.rt1a.//5.0e-27:154:98//Z65369
- 25 F-NT2RP2004425
- F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196:65//AL021530
- 30 F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388
- F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591
- 35 F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815:57//AL034556
- 40 F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890
- 45 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163
- F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85 :484:91//AQ239555
- 50 F-NT2RP2004568//H.vulgare GAA-satellite DNA.//2.0e-07:292:62//Z50100
- 55 F-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755

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F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene,  
partial cds.//1.0:344:56//AF092908

5 F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone  
nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020

F-NT2RP2004600

10 F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete  
sequence.//0.12:109:73//AC005176

15 F-NT2RP2004614

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:  
98//AJ006291

20 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:  
98//AB007929

25 F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE,  
33 unordered pieces.//0.092:239:61//AC005805

30 F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3.  
Contains an EST and GSSs, complete sequence.//1.0:236:61//AL031312

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:  
94//AB014525

35 F-NT2RP2004709//HS\_2033\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-  
15:187:74//AQ230714

40 F-NT2RP2004710//HS\_3185\_82\_D07\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-  
10:110:84//AQ172885

45 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:  
96//AB007947

50 F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:  
71//Z78022

55 F-NT2RP2004767//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65c11,  
reverse read cpg65c11.rt1a.//1.3e-24:217:81//Z62210

F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-

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45:541:71//AF024636

5 F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398

10 F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid screen.//5.0e-53:353:84//U56252

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953 F-NT2RP2004802

15 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179

20 F-NT2RP2004841//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531:84//Z72519

25 F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040O17bA3, genomic survey sequence.//0.96:183:64//AL025645

30 F-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//4.8e-142:710:96//AC004383

F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144

35 F-NT2RP2004936

40 F-NT2RP2004959//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183

45 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-59:339:79//U56732

50 F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-19:187:72//U91328

F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551

55 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029



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F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:273:61//B12642

5 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478

F-NT2RP2004999

10

F-NT2RP2005000//Rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375

15 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515

F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200

20 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141

25 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//AC004849

F-NT2RP2005020

30 F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-43:98:93//AC000380

35 F-NT2RP2005031//HS\_2052\_B2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464

40 F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454

45 F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//0.20:519:57//AC005696

F-NT2RP2005108

50 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564

55 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//X98743

F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//0.00024:547:59//AJ223012

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- 5 F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//0.95:191:62//AC004527
- F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583
- 10 F-NT2RP2005147//HS\_3184\_A1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226
- 15 F-NT2RP2005159//H.sapiens CpG island DNA genomic Mse1 fragment, clone 132g6, forward read cpg132g6.ft1a.//1.1e-13:93:97//Z59162
- F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070
- 20 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125 :633:96//AJ007509
- 25 F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:60//U80808
- F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//AC005189
- 30 F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536
- 35 F-NT2RP2005254
- F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513
- 40 F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666
- 45 F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335
- F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//AF060219
- 50 F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590
- 55 F-NT2RP2005293//HS\_3245\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454

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- 5 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576
- F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//U11701
- 10 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//0.39:353:62//AF032387
- 15 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138
- F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//Z92844
- 20 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247
- 25 F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358
- F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184
- 30 F-NT2RP2005407
- F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:62//AC005346
- 35 F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//4.0e-107:532:97//AQ055548
- 40 F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865
- 45 F-NT2RP2005457//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647
- 50 F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679
- 55 F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//6.5e-18:152:75//AC006116
- F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-

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- 36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo)gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBPII, TNF-R2, CD120B, TNFBR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat polymorphism, complete sequence.//4.4e-12:89:97//AL031276
- 5
- F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//AC004130
- 10
- F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.2e-115:228:99//AC006030
- 15
- F-NT2RP2005491//HS\_2253\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234:80//AQ116847
- 20
- F-NT2RP2005495
- F-NT2RP2005496//HS\_3064\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097
- 25
- F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931
- 30
- F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//0.86:183:63//AC005880
- 35
- F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695
- F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:444:92//AF092563
- 40
- F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307
- 45
- F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993
- 50
- F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449
- 55
- F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963
- F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:

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89//AF046734

- 5 F-NT2RP2005555//HS\_2188\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-  
05:195:65//AQ086723
- 10 F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate  
phosphohydrolase mRNA, complete cds.//2.5e-44:473:71//AF062529
- 15 F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete  
sequence.//0.99:213:65//AC005016
- 20 F-NT2RP2005600//H.sapiens CpG island DNA genomic Mse1 fragment, clone 172d12,  
reverse read cpg172d12.rt1a.//0.32:134:63//Z57359
- 25 F-NT2RP2005605
- F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:  
97//AF062085
- 30 F-NT2RP2005622
- F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:  
61//U10556
- 35 F-NT2RP2005637//NATI (NATI\*10)=acetyltransferase 1 {3' region, polyadenylation  
polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:  
65//S78829
- F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980
- 40 F-NT2RP2005645//HS\_2201\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:  
159:65//AQ066763
- 45 F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493
- 50 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:  
62//AB006626
- F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:  
98//AF064605
- 55 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete  
cds.//2.4e-94:462:98//AF089814

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- F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405
- 5 F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836
- 10 F-NT2RP2005694
- F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPC111-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183
- 15 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342
- 20 F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603
- F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367
- 25 F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528
- F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627
- 30 F-NT2RP2005732//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017
- 35 F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270
- F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342
- 40 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF068868
- 45 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516
- 50 F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853
- F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849
- 55 F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836

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F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//D11336

5 F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds//0.96:184:60//AB015853

10 F-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423

F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579

15 F-NT2RP2005812

20 F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103

F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086

25 F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873

30 F-NT2RP2005853//RPCI11-24D4.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490

35 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564

40 F-NT2RP2005859//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553

F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic survey sequence.//7.8e-06:92:79//AL027276

45 F-NT2RP2005886//HS\_3187\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885

50 F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-32:660:66//L11316

F-NT2RP2005901//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, reverse read cpg15b5.rt1a.//0.0026:66:84//Z54729

55 F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241

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- F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840
- 5 F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770
- 10 F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//1.0e-48:533:71//AC005207
- 15 F-NT2RP2006023//HS\_3048\_A1\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553
- 20 F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912
- F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds.//1.9e-05:418:59//U19495
- 25 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861
- 30 F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047
- F-NT2RP2006071
- 35 F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//AF027207
- 40 F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073
- F-NT2RP2006103//HS\_2254\_A2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602
- 45 F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//11.2e-62:655:71//AC000378
- 50 F-NT2RP2006141//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405
- 55 F-NT2RP2006166//Homo sapiens chromosome 4 clone B3218, complete sequence.//3.1e-45:387:81//AC004063
- F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell



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line point mutant mRNA, complete cds.//0.99:111:73//U62587

- 5 F-NT2RP2006186//Homo Sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554
- 10 F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232
- F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057
- 15 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484
- F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.0e-18:118:97//AQ012480
- 20 F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//7.6e-102:635:86//U49055
- 25 F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-9N9, genomic survey sequence.//8.6e-05:181:63//B71615
- 30 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630
- F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257
- 35 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262
- 40 F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851
- F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//AC003973
- 45 F-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532
- 50 F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893
- 55 F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514
- F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey

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sequence.//7.8e-06:148:70//AL029590

5 F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2  
Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete  
sequence.//6.8e-06:167:70//AL022727

10 F-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
Y313F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808

F-NT2RP2006441

15 F-NT2RP2006454//Sequence 8 from Patent WO9517522.//2.9e-06:180:66//A45338

F-NT2RP2006456

20 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//AJ006266

F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-  
ch4 and secretion domains, partial cds.//0.061:201:66//U50149

25 F-NT2RP2006472

30 F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-  
22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains  
STSs, GSSs and a CA repeat polymorphism, complete sequence.//8.8e-10:273:66//Z93929

35 F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon  
6.//0.71:174:59//U40965

40 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP)  
mRNA, complete cds.//6.6e-114:669:90//AF038966

F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone  
B2-1.//6.0e-26:503:63//M20855

45 F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome.//0.44:134:  
71//U60315

50 F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:  
85//U50537

55 F-NT2RP3000002//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-  
32:214:89//U14571

F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-  
136:637:98//AJ011972

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- 5 F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320
- F-NT2RP3000047
- 10 F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//1.0e-67:626:74//M27877
- F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227
- 15 F-NT2RP3000068
- F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301:61//AC004746
- 20 F-NT2RP3000080//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//1.9e-44:297:79//AL021391
- 25 F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536
- 30 F-NT2RP3000092//RPCI11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22M5, genomic survey sequence.//3.3e-27:157:97//B84237
- 35 F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds.//0.92:185:64//L29260
- F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286:89//AC005189
- 40 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849:98//AB011164
- 45 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//4.2e-24:155:94//AC005884
- 50 F-NT2RP3000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269:81//AL023583
- F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405:57//L39063
- 55 F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence.//0.96:608:55//AC004716

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- F-NT2RP3000220
- 5 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509:58//AF059569
- 10 F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence.//3.5e-05:224:65//AC004101
- 15 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691:86//D86972
- F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence.//0.20:119:68//Z70213
- 20 F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence.//9.8e-78:174:88//AF065393
- 25 F-NT2RP3000255
- F-NT2RP3000267
- 30 F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds.//5.9e-48:374:82//U48853
- 35 F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds.//4.9e-22:583:63//J02932
- F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107
- 40 F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090
- 45 F-NT2RP3000333//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533
- 50 F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181
- F-NT2RP3000348
- 55 F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174:88//AF065393

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F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757

5 F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743

10 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//L04966

15 F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318

F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642

20 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185

25 F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053\_B\_8, complete sequence.//7.9e-53:817:68//AC006083

30 F-NT2RP3000433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681

F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471

35 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488

40 F-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650

45 F-NT2RP3000451//HS\_2024\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=I, genomic survey sequence.//0.011:367:57//AQ229420

50 F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548

55 F-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353

F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440

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F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667

5 F-NT2RP3000526//Homo sapiens full-length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071

10 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966

15 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260

F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554

20 F-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//9.0e-171:827:98//AC006012

25 F-NT2RP3000562

F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

30 F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597

35 F-NT2RP3000584

F-NT2RP3000590//H.sapiens CpG island DNA genomic Mse1 fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723

40 F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868

45 F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305

50 F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320

55 F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128

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F-NT2RP3000622//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-  
29:238:85//AQ175104

5

F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:  
80//AC004890

10

F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21.  
Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein  
L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313

15

F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:  
79//U71363

20

F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//5.2e-46:421:77//AC005089

F-NT2RP3000661

25

F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-  
13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-  
inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced  
novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two  
putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:  
65//AL022237

30

F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961

35

F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:  
141:65//Z77872

40

F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:  
96//D50930

45

F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65)  
mRNA, complete cds.//1.1e-46:622:67//AF015264

50

F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-  
37:429:70//U16655

F-NT2RP3000753

55

F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:  
519:69//Z99281

F-NT2RP3000815//HS\_2237\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D

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Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252

- 5 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387
- 10 F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513  
F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4.//0.69:563:57//M29009
- 15 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062
- 20 F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581
- 25 F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938
- F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082
- 30 F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE
- 35 gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast. plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940
- 40 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831
- 45 F-NT2RP3000865
- F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445
- 50 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367
- 55 F-NT2RP3000875//HS\_2236\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007



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F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//AF021340

5 F-NT2RP3000904//Rat Na<sup>+</sup> channel mRNA, 3' end.//3.6e-106:505:99//M27223

F-NT2RP3000917//Mouse mRNA for Dhml protein, complete cds.//3.1e-132:691:93//D38517

10 F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//3.2e-97:585:88//AF015264

15 F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:89//U91326

F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335

20 F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529

25 F-NT2RP3001004//H.sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cpg39c1.rt1a.//15.9e-27:150:99//Z60925

30 F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:610:57//AC006039

35 F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653

F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927

40 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//AF060219

45 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325

50 F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey sequence.//3.4e-37:222:93//AQ021278

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969

55 F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//AC005317

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F-NT2RP3001111

5 F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871

10 F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//AC005189

15 F-NT2RP3001116//HS\_3075\_A1\_F01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581

20 F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-121:598:97//AL031864

F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367

25 F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:64//Z49078

30 F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//AF027735

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305

35 F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-3M16, genomic survey sequence.//2.1e-15:106:96//B48859

40 F-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266

45 F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, complete sequence.//1.1e-69:207:97//AL034351

50 F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507

55 F-NT2RP3001216//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-05:561:56//AC004845

F-NT2RP3001221

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F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120:87//D12619

5 F-NT2RP3001236

F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396

10

F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey sequence.//8.5e-70:337:100//AQ242007

15 F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430

20 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269

25 F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513

F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101

30 F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561

35 F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//5.9e-39:304:70//AC005837

40 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457

F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465

45 F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709

50 F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790

F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966

55 F-NT2RP3001339//Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935

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F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105

5 F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052

F-NT2RP3001356

10

F-NT2RP3001374

15 F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628

F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332

20

F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198

25 F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296

30 F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046

F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//5.4e-20:245:73//AC005521

35

F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031

40 F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327

45 F-NT2RP3001426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447

F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997

50

F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//8.5e-73:431:91//U69668

55 F-NT2RP3001432//HS\_3032\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619

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F-NT2RP3001447

5 F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase  
10 Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1).  
15 Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282

F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR),  
20 phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065

F-NT2RP3001457

25

F-NT2RP3001459

F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836  
30

F-NT2RP3001490

35 F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395

40 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//8.5e-171:804:98//AF064801

45 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete, cds.//8.9e-140:743:91//U36499

F-NT2RP3001529//Streptomyces griseus DNA for ribosoma protein L21, ribosomal protein L27, Obg, complete cds.//2.1e-14:517:59//D87916

50 F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:63//AF078176

55 F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//4.3e-17:332:67//M83196

F-NT2RP3001580//RPCI11-91E19.TV RPCI11 Homo sapiens genomic clone R-91E19,

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genomic survey sequence.//4.2e-15:110:91//AQ281332

F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104

5

F-NT2RP3001589//RPCI11-68M15.TK RPCI11 Homo sapiens genomic clone R-68M15, genomic survey sequence.//8.7e-108:517:98//AQ237629

10

F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//1.0e-09:257:65//AC004674

15

F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane monooxygenase A beta chain and methane monooxygenase component C genes, complete cds.//0.59:450:57//M90050

20

F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.8e-42:278:79//AL021808

25

F-NT2RP3001629

F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978

30

F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117

35

F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449

40

F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-38:542:66//U49793

45

F-NT2RP3001676//HS\_3090\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250

50

F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358

55

F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//2.8e-130:355:96//AB020860

F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2

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mRNA, complete cds.//2.1e-37:512:70//AF059273

5 F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9,  
genomic survey sequence.//2.8e-19:123:95//AQ012480

F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9-4e-11:167:74//D31962

10 F-NT2RP3001708//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4g7, reverse  
read cpg4g7.rt1d.//1.3e-17:113:97//Z61312

15 F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X99642

F-NT2RP3001716

20 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA,  
complete cds.//1.4e-159:565:97//AF054177

25 F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)-mRNA, partial  
cds.//1.7e-132:786:88//AF008554

F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811:78//D50918

30 F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR  
Region, complete sequence.//6.5e-07:178:69//AC000097

35 F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4  
Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete  
sequence.//5.2e-31:311:77//AL031311

F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//I62381

40 F-NT2RP3001764//Sequence 6 from Patent WO9706245.//6.4e-47:673:66//A59888

F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39644

45 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.8e-151:710:  
98//AB007928

50 F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial  
cds.//1.2e-26:213:85//U13262

55 F-NT2RP3001799//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
469D22, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284

F-NT2RP3001819//S.glaucescens genes strU, strX, strV and strW for 5'-hydroxystreptomycin  
prduction and transport polypeptides.//0.084:526:58//X89010

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- 5 F-NT2RP3001844//HS\_3110\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence.//1.5e-  
40:232:82//AQ140433
- 10 F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//AC005505
- F-NT2RP3001855//Mus musculus homeobox protein PKNX1 (Pknx1) mRNA, complete  
cds.//2.7e-39:575:67//AF061270
- 15 F-NT2RP3001857//M.musculus tex292 mRNA (5'region).//8.7e-07:106:81//X80434
- F-NT2RP3001896
- 20 F-NT2RP3001898//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733
- F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence.//0.58:482:  
25 56//Z73969
- F-NT2RP3001926//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557
- 30 F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete  
sequence.//3.1e-28:263:77//AC004651
- 35 F-NT2RP3001931
- F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8,  
genomic survey sequence.//3.6e-24:182:91//B95475
- 40 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:  
96//AB014575
- 45 F-NT2RP3001944
- F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING  
DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844
- 50 F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1  
(o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6),  
chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-  
55 10:564:60//AF030694
- F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains



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ESTs.//2.5e-57:361:80//Z83822

- 5 F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//AR025386
- F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137
- 10 F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640
- F-NT2RP3002033//H.sapiens DNA sequence.//0.012:214:63//Z22493
- 15 F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773
- 20 F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841
- F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249
- 25 F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682
- 30 F-NT2RP3002062
- F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.24:508:58//AJ235272
- 35 F-NT2RP3002081//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494
- 40 F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//9.6e-66:562:77//AC006210
- 45 F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040
- 50 F-NT2RP3002108
- F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020
- 55 F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:60//AF003370

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- 5 F-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710
- F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742
- 10 F-NT2RP3002163
- F-NT2RP3002165//M.musculus HCNGP mRNA.//1.4e-142:867:87//X68061
- 15 F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//0.090:394:59//AC006121
- 20 F-NT2RP3002173//HS\_3062\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219
- 25 F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808
- 30 F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321
- 35 F-NT2RP3002248//HS\_3029\_A1\_D10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880
- 40 F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321
- 45 F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004
- 50 F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898
- F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810
- 55 F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504

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F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862

5 F-NT2RP3002343//HS\_3010\_A2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068

10 F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396

15 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.4e-190:911:98//AB018331

20 F-NT2RP3002399

25 F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578

30 F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927

35 F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence.//0.00020:170:65//Z49068

40 F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence.//1.6e-59:308:97//AF091088

45 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246

F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272

50 F-NT2RP3002549//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-26:123:72//AC004821

55 F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds.//0.76:459:59//U60418

F-NT2RP3002587//Homo sapiens chromosome Y, clone 264,M,20, complete

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sequence.//4.6e-13:199:76//AC004617

- 5 F-NT2RP3002590//Porphyra purpurea chloroplast, complete genome.//0.88:284:60//U38804
- F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence.//2.0e-22:140:95//B68331
- 10 F-NT2RP3002603
- F-NT2RP3002628//C.acetobutylicum dnaJ and orfB genes.//2.0e-05:333:60//X69050
- 15 F-NT2RP3002631
- F-NT2RP3002650//Mus musculus mRNA for cartilage-associated protein (CASP).//1.5e-20:641:62//AJ006469
- 20 F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59//Z78205
- F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from 7q31.2-q31, complete sequence.//0.98:453:57//AC004946
- 25 F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence.//3.3e-22:407:67//AC006129
- 30 F-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.0e-12:336:66//AL023704
- F-NT2RP3002682//Caenorhabditis elegans cosmid F17C11, complete sequence.//1.3e-21:448:64//Z72507
- 35 F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence.//2.5e-25:173:91//B51656
- 40 F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.2e-73:728:74//D17577
- 45 F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey sequence.//0.0012:55:92//AQ263530
- 50 F-NT2RP3002713
- F-NT2RP3002763//Caenorhabditis elegans cosmid T20F10, complete sequence.//0.98:209:63//Z81594
- 55 F-NT2RP3002770
- F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA,

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alternatively spliced short variant, partial cds.//0.78:515:57//AF029325

- 5 F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718
- 10 F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//0.32:187:66//AC005549
- 15 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715
- 20 F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4.//4.2e-05:226:65//U64601
- F-NT2RP3002869//Mus musculus semaphorin V1a mRNA, complete cds.//2.0e-93:638:83//AF030430
- 25 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895
- 30 F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087
- F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314
- 35 F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815
- 40 F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500
- F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754
- 45 F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024
- 50 F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666
- F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820
- 55 F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505

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F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644

5 F-NT2RP3002988//HS\_3015\_A1\_B07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708

10 F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF109905

15 F-NT2RP3003032//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-80, complete sequence.//1.6e-08:809:58//AL010153

20 F-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//U78090

F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1).//1.4e-12:633:59//X16609

25 F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410

30 F-NT2RP3003071//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.rt1c.//6.8e-15:95:100//Z64565

F-NT2RP3003078

35 F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//8.1e-72:732:71//D88315

40 F-NT2RP3003121

F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//AC004510

45 F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//D12646

50 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//U17995

55 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639

F-NT2RP3003150

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F-NT2RP3003157//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-  
92:493:94//AQ155489

5

F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1  
mRNA, complete cds.//8.6e-06:228:65//AF064868

10

F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933

F-NT2RP3003197

15

F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65)  
mRNA, complete cds.//4.1e-48:640:67//AF015264

20

F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:  
81//U31059

F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799

25

F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA,  
complete cds.//6.3e-75:776:74//U20286

30

F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:  
74//AJ006064

35

F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:  
617:98//AF055460

F-NT2RP3003251//H.sapiens Staf50 mRNA.//3.5e-67:651:76//X82200

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F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153

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F-NT2RP3003278//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward  
read cpg28b4.ft1a.//4.0e-27:174:93//Z60555

F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:  
93//L36983

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F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete  
cds.//1.7e-64:662:71//AF004162

55

F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete  
cds.//4.9e-37:682:64//D85610

F-NT2RP3003302//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.6e-95:680:

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82//AC006213

- 5 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//1.0:191:62//AC004527
- F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107
- 10 F-NT2RP3003327//H.sapiens Staf50 mRNA.//2.5e-29:253:67//X82200
- F-NT2RP3003330
- 15 F-NT2RP3003344
- F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//9.0e-41:296:84//AC005284
- 20 F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).//0.047:404:60//AL021069
- 25 F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//8.3e-122:632:96//AC005519
- F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//0.0036:127:74//AC000360
- 30 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874
- 35 F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407
- F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:63//U90653
- 40 F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//AF071317
- 45 F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173
- 50 F-NT2RP3003433//HS\_2219\_B2\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866
- 55 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828



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F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268

5 F-NT2RP3003491//CIT-HSP-2344O1.TR CIT-HSP Homo sapiens genomic clone 2344O1, genomic survey sequence.//1.2e-39:213:97//AQ057124

10 F-NT2RP3003500//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347

15 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:60//AC004234

20 F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049

F-NT2RP3003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985

25 F-NT2RP3003564//HS\_3141\_B1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798

30 F-NT2RP3003572

35 F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632

F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387

40 F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235

45 F-NT2RP3003625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600

F-NT2RP3003656

50 F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

55 F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096

F-NT2RP3003672

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- 5 F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, -9 unordered pieces.//3.4e-16:425:64//AC005811
- 10 F-NT2RP3003686//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993
- F-NT2RP3003701
- 15 F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:788:82//U42975
- 20 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300
- 25 F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785
- 30 F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGRIB, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326
- 35 F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458
- 40 F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031
- 45 F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321
- F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801
- 50 F-NT2RP3003819
- F-NT2RP3003825
- 55 F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626
- F-NT2RP3003831//RPC11-50N15.TJ RPC11 Homo sapiens genomic clone R-50N15,

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genomic survey sequence.//1.1e-21:174:85//AQ082633

- 5 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070611
- 10 F-NT2RP3003842//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884
- F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268
- 15 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343
- 20 F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181
- 25 F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554
- F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//2.6e-47:404:77//AF057358
- 30 F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504
- 35 F-NT2RP3003989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661
- F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds.//0.021:433:58//U58837
- 40 F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4e-164:838:94//X84692
- 45 F-NT2RP3004016//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726
- 50 F-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400
- 55 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317
- F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold

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hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484:62//AL021939

- 5 F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA.//1.9e-102:684:83//X76089
- F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207:63//B09433
- 10 F-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.5e-25:272:77//AC005038
- 15 F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223:73//AC003973
- F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds.//2.2e-28:637:63//AF000560
- 20 F-NT2RP3004145
- 25 F-NT2RP3004148
- F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578:98//AF032900
- 30 F-NT2RP3004189//M.musculus tex292 mRNA (5'region).//1.1e-06:102:82//X80434
- F-NT2RP3004206//D.melanogaster crn mRNA.//7.3e-69:715:71//X58374
- 35 F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650:66//D64009
- 40 F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//8.4e-55:184:84//D42052
- F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//0.22:458:60//AC006084
- 45 F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence.//1.6e-29:409:69//Z22181
- 50 F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//3.6e-117:242:100//AC005385
- 55 F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//X69353
- F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489:91//AF013967

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- 5 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982
- F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871
- 10 F-NT2RP3004332
- F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase.//0.23:501:57//X80908
- 15 F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020
- 20 F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877
- F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025
- 25 F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23 :352:67//AC005653
- F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249
- 35 F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678
- F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206
- 40 F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326
- 45 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917
- F-NT2RP3004466//HS\_3038\_B2\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458
- 50 F-NT2RP3004470//H.sapiens CpG island DNA genomic MseI fragment, clone 81a11, reverse read cpg81a11.rt1a.//7.0e-25:148:96//Z56029
- 55 F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5,

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genomic survey sequence.//1.6e-20:143:92//AQ052792

5 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925

10 F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//U47024

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851

15 F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//4.0e-67:265:84//AC006023

20 F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.2e-55:415:78//AC004673

F-NT2RP3004504//M.musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260

25 F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//AC005328

30 F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574

F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316

35 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532

40 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126

45 F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emzf1) mRNA, complete cds.//6.9e-18:433:64//AF031955

F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780

50 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//AF026445

55 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946

F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266

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- 5 F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-14:360:65//AC004977
- F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:73//AF005355
- 10 F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.046:437:57//S69350
- 15 F-NT2RP3004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882
- F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//1.5e-155:844:92//AC006121
- 20 F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//0.012:417:59//AB012242
- 25 F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//AC005035
- 30 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761
- F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469
- 35 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449
- 40 F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558
- 45 F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538
- 50 F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931
- F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952
- 55 F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776

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- F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681
- 5 F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088
- 10 F-NT2RP4000159//RPCI11-75N16.TJ RPCI11 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551
- 15 F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210
- F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989
- 20 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600
- 25 F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300
- F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261
- 30 F-NT2RP4000218//RPCI11-69B7.TJ RPCI11 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504
- 35 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470
- 40 F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523
- F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092
- 45 F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515
- 50 F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408
- F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481
- 55 F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322



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F-NT2RP4000323

F-NT2RP4000355

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F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281

10

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195

15

F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272

F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//30536

20

F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//4.3e-05:450:58//D63850

25

F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//9.2e-37:336:69//AC006116

F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966

30

F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086

35

F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101

40

F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194

F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183

45

F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982

50

F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499

55

F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483

F-NT2RP4000481

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F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125

5 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904

F-NT2RP4000515

10 F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//1.6e-179:851:98//AC006238

15 F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840

20 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720

F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498

25 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386

F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence.//1.3e-05:498:58//AC002443

30 F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I05465

35 F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580

F-NT2RP4000588//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543

40 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//AF067730

45 F-NT2RP4000638//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333

50 F-NT2RP4000648//Homo sapiens KNXL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335

55 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904

F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:99//AB004852

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- 5 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149
- F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272
- 10 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178
- F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//L19301
- 15 F-NT2RP4000739//CIT-HSP-2010O22.TR CIT-HSP Homo sapiens genomic clone 2010O22, genomic survey sequence.//1.1e-24:161:93//B57903
- 20 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917
- F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U22818
- 25 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939
- 30 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189
- 35 F-NT2RP4000837//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420
- 40 F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6D8, genomic survey sequence.//1.5e-44:281:91//B48216
- F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515
- 45 F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367
- 50 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616
- F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804
- 55 F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//D45913

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- F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901
- 5 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-08:609:58//AC004290
- 10 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975
- 15 F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547
- F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532
- 20 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004688
- 25 F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.0e-128:673:96//AC005519
- 30 F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657
- F-NT2RP4000975//CIT-HSP-2307I6.TF CIT-HSP Homo sapiens genomic clone 2307I6, genomic survey sequence.//6.5e-31:317:79//AQ015742
- 35 F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942
- F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823
- 40 F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911
- 45 F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358
- 50 F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424
- F-NT2RP4001004
- 55 F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176
- F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete

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cds.//2.0e-135:789:89//U67140

5 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete  
cds.//3.7e-120:718:88//U20086

10 F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-  
22:452:64//D89170

F-NT2RP4001057

15 F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:  
639:62//AJ006469

F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124

20 F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018

F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:  
25 628:70//X65372

F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:  
86//AB011164

30 F-NT2RP4001095

F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7,  
35 genomic survey sequence.//9.4e-17:185:79//AQ263402

F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:  
87//M96629

40 F-NT2RP4001122

F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete  
45 cds.//4.2e-17:636:61//U82668

F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete  
sequence.//2.5e-23:408:60//AC004969

50 F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079

F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1  
55 unordered pieces.//2.7e-116:684:89//AC005095

F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete  
cds.//3.0e-48:581:66//D67067

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- 5 F-NT2RP4001150//Homo sapiens alone DJ1032D07, WORKING DRAFT SEQUENCE, 3  
unordered pieces.//9.4e-25:193:67//AC004952
- F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476
- 10 F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429  
nt].//0.0014:187:67//S74494
- F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rscI9) mRNA,  
partial cds.//0.032:453:58//U82511
- 15 F-NT2RP4001207//HS\_2248\_A1\_C03\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey  
sequence.//0.00018:58:94//AQ192358
- 20 F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019O18 map  
10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877
- 25 F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant,  
complete cds.//3.6e-44:187:74//U37251
- 30 F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:  
288:67//AL032657
- F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-  
26:855:60//AF059569
- 35 F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-  
18E11, genomic survey sequence.//2.7e-15:101:98//B88081
- 40 F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase  
(rifD) gene, complete cds.//1.0:459:59//U33061
- 45 F-NT2RP4001260//Sequence 2 from Patent WO9601901.//0.0018:246:63//A48324
- F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201:67//AC005854
- 50 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15,  
genomic survey sequence.//3.5e-18:138:92//AQ040728
- F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA,  
nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535:65//AF043250
- 55 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-  
145:795:91//AJ001119

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5 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21,  
genomic survey sequence.//8.4e-16:109:94//B89870

10 F-NT2RP4001339//HS\_3205\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence.//7.1e-  
24:305:73//AQ183725

15 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete  
sequence.//1.9e-17:106:91//AC004918

20 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631:  
66//X91011

F-NT2RP4001351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608:64//AL031428

F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540:57//AL031107

25 F-NT2RP4001372//RPC11-49L11.TJ RPC11 Homo sapiens genomic clone R-49L11,  
genomic survey sequence.//8.5e-23:129:100//AQ051701

30 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213:61//X78609

F-NT2RP4001375

35 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311\_F\_12, complete  
sequence.//7.3e-28:153:88//AC005722

F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete  
sequence.//7.2e-47:518:73//AC004691

40 F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.00079:686:  
57//J03998

45 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds.//2.0e-76:818:71//D86957

F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5e-87:839:73//X78933

50 F-NT2RP4001442

F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218:  
63//AB018326

55 F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-  
14:109:90//J49884

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- 5 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480:75//D10523
- F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392:72//AF049612
- 10 F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat.//2.7e-24:147:96//X61693
- 15 F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds.//0.87:583:58//M32513
- 20 F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.93:394:58//AC005308
- F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820:89//U20086
- 25 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w.//2.2e-05:319:61//Z71663
- 30 F-NT2RP4001551//S.pombe chromosome II p1 p8B7.//0.64:335:60//AL032684
- F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:309:58//AC004806
- 35 F-NT2RP4001567//HS\_2166\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence.//0.99:188:59//AQ086290
- 40 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566:72//D79989
- 45 F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F20, genomic survey sequence.//2.8e-19:119:97//B85885
- F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop.//5.8e-129:813:85//X92987
- 50 F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-131:795:86//AJ223830
- F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase.//1.3e-14:663:59//X74219
- 55 F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:135:73//AC002364



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- 5 F-NT2RP4001614//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.4e-  
06:78:89//AQ099333
- F-NT2RP4001634
- 10 F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo  
sapiens genomic clone cSRL-161F1, genomic survey sequence.//4.9e-12:144:76//B02870
- 15 F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:  
437:86//Y11092
- 20 F-NT2RP4001656//HS\_2013\_A1\_D01\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-  
30:207:89//AQ224793
- F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:71//L49362
- 25 F-NT2RP4001679//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
462O23, WORKING DRAFT SEQUENCE.//2.7e-45:351:84//AL031431
- 30 F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete  
sequence.//1.8e-30:163:88//U96629
- 35 F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)),  
complete sequence.//1.1e-13:402:63//AC004296
- F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-  
37M21, genomic survey sequence.//0.88:177:67//AQ029840
- 40 F-NT2RP4001739
- F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read  
12QTELOO023.seq.//4.9e-36:192:98//Z96232
- 45 F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316
- 50 F-NT2RP4001790//Homo sapiens clone NH0569I24, complete sequence.//1.4e-29:327:  
74//AC005678
- F-NT2RP4001803
- 55 F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-  
16:576:60//AF054841

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F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence.//2.1e-08:601:59//Z98743

5

F-NT2RP4001828

F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:73//D31888

10

F-NT2RP4001841

F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572

15

F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691

20

F-NT2RP4001889//HS\_2052\_B1\_H06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425

25

F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//AC005014

30

F-NT2RP4001896//T3B4TFC TAMU Arabidopsis thaliana genomic clone T3B4, genomic survey sequence.//0.99:354:61//B26193

35

F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//0.031 :409:60//AB011413

40

F-NT2RP4001927//HS\_2216\_B1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677

F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046

45

F-NT2RP4001946//HS\_3021\_B2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185

50

F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-18:421:65//AL022577

55

F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14,

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genomic survey sequence.//0.030:358:61//AQ005028

5 F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485

10 F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.9e-57:555:75//AC003976

15 F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950 F-NT2RP4002047//Saccharomyces cerevisiae chromosome XII cosmid 8003.//1.6e-29:520:64//U17243

20 F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//2.8e-22:137:96//B80243

F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//0.019:141:65//AQ248640

25 F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223

30 F-NT2RP4002075//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841

35 F-NT2RP4002078//RPC111-73M20.TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030

F-NT2RP4002081//F.rubripes GSS sequence, clone 190O22bB9, genomic survey sequence.//0.0024:350:60//Z92062

40 F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437

45 F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515

F-NT2RP4002791

50 F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383

55 F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//6.5e-91:672:83//AC004662

F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197

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- 5 F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901
- F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380
- 10 F-NT2RP5003492
- F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365
- 15 F-NT2RP5003506//H.sapiens CpG island DNA genomic Mse1 fragment, clone 71h2, reverse read cpg71h2.ft1a.//1.4e-49:283:93//Z62703
- 20 F-NT2RP5003512//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312
- 25 F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236
- 30 F-NT2RP5003524//Homo sapiens beta-spectrin (HSpTB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178
- F-NT2RP5003534//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14c10, forward read cpg14c10.ft1b.//0.00013:70:91//Z54631
- 35 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934
- 40 F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510
- 45 F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933
- F-OVARC1000013
- 50 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922
- 55 F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674
- F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603

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F-OVARC1000058

5 F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625

10 F-OVARC1000068//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883

15 F-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387

20 F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259

25 F-OVARC1000087//HS\_2004\_B2\_E11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037

30 F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489

F-OVARC1000092//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.1e-10:720:58//AC004617

35 F-OVARC1000106//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369

40 F-OVARC1000109

45 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

F-OVARC1000114//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574

50 F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027

55 F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640

F-OVARC1000145//HS\_2257\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-

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30:203:90//AQ304854

5 F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22,  
genomic survey sequence.//1.1e-26:146:100//AQ056703

F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695

10 F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete  
sequence.//4.9e-19:381:63//AC005764

15 F-OVARC1000191//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557

20 F-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4,  
BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered  
pieces.//6.4e-161:781:97//AC004604

25 F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete  
cds.//9.2e-33:511:65//AF068332

F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey  
sequence.//1.1e-13:139:79//AL019910

30 F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I81226

F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete  
cds.//1.1e-112:697:87//AF060194

35

F-OVARC1000288 2.2e-22:181:83//J00345

40 F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-192A9, genomic  
survey sequence.//4.8e-18:110:99//B18003

F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574

45 F-OVARC1000309

F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//3.1e-122:325:95//AC005236

50

F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA,  
complete cds.//4.0e-46:339:84//U19614

55 F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696

F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:

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59//AC005007

- 5 F-OVARC1000384//Homo sapiens expanded SCA7 CAG repeat.//2.2e-09:276:64//AF020275
- F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693
- 10 F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201
- 15 F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166
- F-OVARC1000420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718
- 20 F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826
- 25 F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558
- F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165
- 30 F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284
- F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678
- 35 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583
- 40 F-OVARC1000461
- 45 F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//4.7e-124:650:93//AF023451
- F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//1.0e-15:510:59//AC004221
- 50 F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence.//2.5e-06:272:62//AJ227191
- 55 F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829

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- 5 F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuroneurin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//1.7e-13:709:60//Z99297
- 10 F-OVARC1000496//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031733
- 15 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:539:99//AF051850
- 20 F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.0e-149:716:98//AC005024
- 25 F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510
- 30 F-OVARC1000543//HS\_3055\_A2\_F10\_MF CIT Approved Human Genomic\_Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence.//0.19:104:71//AQ102820
- 35 F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.4e-136:670:97//AL022069
- 40 F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//1.3e-15:262:69//AC002985
- 45 F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733
- 50 F-OVARC1000573//HS\_3241\_B1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942
- 55 F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.7e-97:445:90//AC002414
- F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1 e-27:354:72//AC003973
- F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containg transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete



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sequence.//0.97:276:62//AL023775

F-OVARC1000605

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F-OVARC1000622//Homo sapiens (subclone 2\_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648

10

F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069

15

F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772

20

F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162

F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244

25

F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713

30

F-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424

35

F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.5e-151:549:99//AF027156

F-OVARC1000689//nbxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003

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F-OVARC1000700

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F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925

F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661

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F-OVARC1000730

F-OVARC1000746

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F-OVARC1000769//HS\_2056\_B2\_G06\_T7 CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence.//8.8e-19:147:86//AQ245905

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- F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403
- 5 F-OVARC1000781//Sequence 5 from Patent WO9722695.//1.9e-89:705:78//A63552
- F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete  
sequence.//3.0e-131:631:98//AC004542
- 10 F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete  
sequence.//1.7e-32:295:80//AC003691
- 15 F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT  
SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469
- F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:  
20 94//Y17711
- F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:  
100//AB014543
- 25 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584
- F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963
- 30 F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125
- F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete  
35 cds.//2.2e-08:98:88//U20086
- F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//0.25:231:  
40 61//Z82044
- F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6,  
genomic survey sequence.//0.00035:139:69//B89721
- 45 F-OVARC1000890
- F-OVARC1000891
- 50 F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-  
12.3. Contains part of a Homeobox domain containing gene and GSSs, complete  
sequence.//1.4e-18:473:64//AL024494
- 55 F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein  
(BICP4) gene, complete cds.//8.9e-08:378:63//L14320

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F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172

5 F-OVARC1000924//HS\_2022\_A1\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493

10 F-OVARC1000936//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.2e-113:476:91//AC003983

15 F-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848

20 F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549

F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276

25 F-OVARC1000959//CIT-HSP-2348O16.TR CIT-HSP Homo sapiens genomic clone 2348O16, genomic survey sequence.//0.99:270:59//AQ062850

30 F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.9e-41:577:72//AL009181

35 F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270

F-OVARC1000971//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841

40 F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274

F-OVARC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858

45 F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785

50 F-OVARC1001000//HS\_2247\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=O, genomic survey sequence.//3.1e-60:315:96//AQ153910

55 F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3:1e-124:595:98//AC004190

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F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290

5 F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021

10 F-OVARC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451

15 F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533

F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149

20 F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081

25 F-OVARC1001044//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//0.0017:387:6.1//AL031319

30 F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112:74//AF053768

F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292

35 F-OVARC1001062//nbxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878

F-OVARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525

40 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657

45 F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529

50 F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153

F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333

55 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897

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- 5 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913
- 10 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782
- 15 F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), complete sequence.//0.99:148:67//AC005178
- 20 F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302:74//AC000382
- 25 F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey sequence.//0.94:106:66//B79052
- F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79//X62322
- 30 F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.9e-90:496:84//AC004069
- 35 F-OVARC1001162
- F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:219:64//AC004961
- 40 F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete genome.//1.0:265:59//AE001141
- 45 F-OVARC1001170//H.sapiens (xs170) mRNA, 350bp.//4.6e-58:355:90//Z36823
- F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey sequence.//1.5e-25:152:83//AQ002315
- 50 F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//0.0024:94:80//AL022323
- 55 F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356:60//AF063001
- F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub II.//0.0062:275:60//X58195
- F-OVARC1001188//Homo sapiens full-length insert cDNA clone ZD93F03.//1.8e-32:180:97//AF086486
- F-OVARC1001200

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- 5 F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence.//0.013:128:67//Z48334
- F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7e-131:811:87//AC001235
- 10 F-OVARC1001243//Human BAC clone GS117O10 from 7q21-q22, complete sequence.//0.044:457:59//AC003078
- 15 F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-18:118:95//M80613
- 20 F-OVARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95 :649:84//AF027505
- F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72:83//U35776
- 25 F-OVARC1001270
- F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543
- 30 F-OVARC1001282//RPC111-60K8.TK RPC111 Homo sapiens genomic clone R-60K8, genomic survey sequence.//0.0089:285:58//AQ195857
- 35 F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018
- 40 F-OVARC1001306//nbxb0002M13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061
- 45 F-OVARC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986
- F-OVARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504
- 50 F-OVARC1001339//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//0.76:89:74//AC006071
- 55 F-OVARC1001341//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402
- F-OVARC1001342

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- 5 F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=O, genomic survey sequence.//1.5e-07:254:67//B44456
- 10 F-OVARC1001357//Homo sapiens Xp22-149 BAC RPCI11-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297
- F-OVARC1001360
- 15 F-OVARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811
- 20 F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801
- F-OVARC1001376//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680
- 25 F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819
- 30 F-OVARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287
- F-OVARC1001399//CIT-HSP-2291I8.TR CIT-HSP Homo sapiens genomic clone 2291I8, genomic survey sequence.//1.7e-11 :104:87//AQ007611
- 35 F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651
- 40 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426
- 45 F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudogene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714
- 50 F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387
- F-OVARC1001442//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687
- 55 F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//Z84482

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F-OVARC1001476//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277

5 F-OVARC1001480

F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140

10

F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507

15

F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039

20

F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411

25

F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219

30

F-OVARC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037

35

F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//2.4e-115:540:99//AF031165

40

F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945

45

F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409

F-OVARC1001611

F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS, complete sequence.//0.022:146:70//AL031682

50

F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.5e-109:358:96//AB005543

55

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393:81//AB006867



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F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence.//0.94:85:69//B92840

5 F-OVARC1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651

10 F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:262:59//U41662

15 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283:65//M57752

F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81//X12650

20 F-OVARC1001745//HS\_3007\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522

25 F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781

F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//4.2e-149:706:98//U97670

30 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580:96//AB014575

35 F-OVARC1001768

F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//AC005066

40 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704

45 F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214:61//AQ264481

50 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//9.5e-151:712:99//AL023694

55 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748

F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete

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sequence.//1.7e-63:526:81//AC003662

5 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS.//0.17:214:65//Z70224

10 F-OVARC1001820//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779

F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//2.8e-17:509:62//AC005609

15 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X.//0.35:403:58//Z73361

20 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence.//2.4e-25:148:96//B94622

25 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122:95//AF070611

30 F-OVARC1001879//HS\_3026\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748

F-OVARC1001880//Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.//3.5e-05:489:60//U51127

35 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-29:350:74//AC005020

40 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749

45 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904

50 F-OVARC1001911//HS\_2196\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069

55 F-OVARC1001916//HS\_3054\_B1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979

F-OVARC1001928

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F-OVARC1001942//H.sapiens CpG island DNA genomic Mse1 fragment, clone 21d7, forward read cpg21d7.ft1a.//7.2e-12:83:98//Z60390

5 F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:69//AF059179

10 F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294:67//U37263

15 F-OVARC1001950//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.5e-20:261:68//AJ011929

F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4.//0.99:447:57//Z19021

20 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//2.9e-19:178:83//AC005995

25 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:232:62//AL034559

F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.1e-158:739:98//AB007934

30 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP000011

35 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-136:683:96//AC006015

40 F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence.//1.0:220:61//AC004668

F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.1e-115:557:98//AF041483

45 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.013:461:57//AC006241

50 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AF016427

F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey sequence.//2.3e-11:258:67//AQ055576

55 F-OVARC1002156

F-OVARC1002158//F17O7-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic

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survey sequence.//1.8e-16:383:66//B11616

5 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosinephosphatase.//0.0041:300:64//X79568

10 F-OVARC1002182//F.rubripes GSS sequence, clone 123I23aA7, genomic survey sequence.//1.4e-10:240:66//AL017241

F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey sequence.//8.2e-10:158:75//AQ003859

15 F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585

F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//3.8e-51:550:72//AF022789

20 F-PLACE1000014

25 F-PLACE1000031//Homo sapiens alone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.91:333:61//AC004821

F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z93023

30 F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//AC005177

35 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508

40 F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154

F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//AC005521

45 F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.2e-09:143:73//AC005848

50 F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence.//0.52:390:60//AC002389

55 F-PLACE1000094

F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//4.4e-129:731:92//AL023580

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F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888

5 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete  
cds.//7.7e-150:737:97//AF058291

10 F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I76211 F-  
PLACE1000213

15 F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic  
sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504

F-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
695O20, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

20 F-PLACE1000246//HS\_2008\_A2\_D04\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:  
153:61//AQ269813

25 F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:  
571:60//U11584

30 F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & amp;  
tRNA-Val.//0.00013:369:59//X54011

F-PLACE1000332//HS\_2016\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-  
35 83:424:96//AQ232106

F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16,  
40 genomic survey sequence.//0.13:46:100//AQ047350

F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA,  
alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891

45 F-PLACE1000380//F.rubripes GSS sequence, clone 047P21aA10, genomic survey  
sequence.//0.43:198:62//Z88163

50 F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial  
cds.//8.7e-149:740:96//U58032

F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds.//0.22:484:  
55 56//D86074

F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:  
372:65//U89867

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- 5 F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.6e-85:421:87//AC005899
- F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515
- 10 F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189
- 15 F-PLACE1000435//HS\_3217\_A2\_A12\_MR CIT Approved Human Genomic-Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698
- 20 F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-61:616:71//AC004382
- 25 F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580
- F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence.//1.1e-33:349:76//AC002491
- 30 F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//U35245
- 35 F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276
- 40 F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484
- 45 F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409
- F-PLACE1000564
- 50 F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//3.3e-46:631:68//M27877
- 55 F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542
- F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449
- F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:

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61//X95276

- 5 F-PLACE1000610//HS\_2056\_A1\_D10\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-  
24:188:87//AQ235967
- 10 F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete  
cds.//2.4e-47:687:66//AF044201
- F-PLACE1000636
- 15 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,  
complete cds.//1.5e-152:747:96//AF102265
- 20 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE  
546750 and LLNLc110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896
- F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675:70//S78219
- 25 F-PLACE1000712
- F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo  
sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:  
30 266:82//B43026
- F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8,  
genomic survey sequence.//0.023:157:68//AQ113109
- 35 F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence.//0.099:664:  
57//AL034559
- 40 F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone  
wg2c3.//0.00068:206:62//X76589
- 45 F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-3J18,  
genomic survey sequence.//6.5e-08:93:89//B63806
- F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:  
50 98//AB014548
- F-PLACE1000786//Drosophila melanogaster cosmid 80H7.//1.4e-43:589:68//AL031027
- 55 F-PLACE1000793//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12,  
reverse read cpg13d12.rt1c.//4.6e-09:71:100//Z64565
- F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete

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sequence.//5.0e-14:235:72//AC002310

5 F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.013:404:60//AC006158

10 F-PLACE1000849//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72a10, reverse read cpg72a10.rt1a.//3.3e-09:82:92//Z62712

F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935

15 F-PLACE1000863//H.sapiens CpG island DNA genomic Mse1 fragment, clone 53d2, forward read cpg53d2.ft1b.//7.3e-37:199:98//Z55621

20 F-PLACE1000909//H.sapiens CpG island DNA genomic Mse1 fragment, clone 173f8, reverse read cpg173f8.rt1a.//1.5e-17:128:92//Z57391

F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181

25 F-PLACE1000948

30 F-PLACE1000972//RPC111-61B1.TJ RPC111 Homo sapiens genomic clone R-61B1, genomic survey sequence.//1.0e-26:148:99//AQ194348

F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572

35 F-PLACE1000979//H.sapiens CpG island DNA genomic Mse1 fragment, clone 76e8, reverse read cpg76e8.rt1a.//2.7e-10:84:94//Z55963

40 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267

45 F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene.//0.0056:443:58//U01011

F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey sequence.//0.99:277:58//B58681

50 F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357

55 F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//AC004741



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F-PLACE1001024

5 F-PLACE1001036//CIT-HSP-2373110.TF CIT-HSP Homo sapiens genomic clone 2373110,  
genomic survey sequence.//1.1e-80:393:98//AQ108662

10 F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K919,  
complete sequence.//8.8e-40:483:66//AB013390

F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate  
reductase/saccharopine dehydrogenase.//1.2e-23:224:80//AJ224761

15 F-PLACE1001076//HS\_2195\_B1\_D05\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:  
168:66//AQ066659

20 F-PLACE1001088

F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:  
96//AF065485

25 F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene,  
partial cds.//0.0073:253:62//U81400

30 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA,  
complete cds.//2.5e-64:676:71//AF022158

35 F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//3.8e-  
26:174:93//M30702

F-PLACE1001168

40 F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-  
23:245:68//AC005603

45 F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3.  
Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker-  
CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat  
protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV).  
Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.010:102:  
50 70//AL031177

F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete  
cds.//9.3e-82:684:77//D14336

55

F-PLACE1001241

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F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219

F-PLACE1001272//H.sapiens subunit of coatmer complex.//0.31:50:96//X70476

5

F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507

10

F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320

F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642

15

F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617

20

F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282

25

F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181

30

F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342

35

F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614

40

F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324

45

F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319

F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340

50

F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177

55

F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:

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365:96//AF091087

5 F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//8.2e-121:608:97//AC006241

10 F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384

F-PLACE1001456//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106

15 F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148

20 F-PLACE1001484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660

25 F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon L//0.00015:333:59//L78720

F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:161:66//AC004373

30 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786

35 F-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667

40 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//2.7e-139:482:96//AC005669

45 F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261

50 F-PLACE1001570//HS\_3105\_A1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817

55 F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//1.8e-102:217:99//AB020860

F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984

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- 5 F-PLACE1001608//HS\_2189\_A1\_G07\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-  
60:429:84//AQ221959
- 10 F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//4.4e-114:552:98//AC005037
- 15 F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-  
13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to  
monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete  
sequence.//0.93:131:71//AL031587
- 20 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:  
75//AB018341
- F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032
- 25 F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete  
sequence.//7.7e-159:788:97//AC005971
- 30 F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11.  
Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a  
pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-  
Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene.  
Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003  
and DXS1055, complete sequence.//7.8e-36:365:73//AL022165
- 35 F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete  
sequence.//9.1e-149:760:96//AC005921
- 40 F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH),  
complete cds.//2.9e-57:643:71//M16200
- 45 F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958\_E\_11, WORKING  
DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883
- F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776
- 50 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC  
Region, complete sequence.//1.0:274:59//AC000051
- 55 F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124
- F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607

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F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221

5 F-PLACE1001745

F-PLACE1001746//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744

10

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243

15 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842

20 F-PLACE1001761//HS\_3027\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972

25 F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394

F-PLACE1001781 1.3e-08:238:65//AC005637

30 F-PLACE1001799//HS\_3075\_B1\_H03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474

35 F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence.//0.00035:196:66//AB020749

40 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953

45 F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286

F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177

50 F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850

55 F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244

F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15,

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genomic survey sequence.//9.3e-08:383:63//AQ194408

F-PLACE1001912

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F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935

10

F-PLACE1001928//HS\_2220\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361

15

F-PLACE1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596

20

F-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755

25

F-PLACE1002004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996

F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337

30

F-PLACE1002052//HS\_2178\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908

35

F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284

40

F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178

45

F-PLACE1002090//Homo sapiens full-length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131

50

F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086

55

F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527

F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1.

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Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162

- 5 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556
- 10 F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539
- 15 F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662
- 20 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805
- 25 F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244
- 30 F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720
- 35 F-PLACE1002213//HS\_3238\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965
- 40 F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800
- 45 F-PLACE1002256//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-72, complete sequence.//0.022:458:59//AL010142
- 50 F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324
- 55 F-PLACE1002319
- F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956
- F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623
- F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//5.6e-05:474:59//AC005922

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- 5 F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928
- F-PLACE1002437//M.musculus abc1 mRNA.//5.5e-62:452:85//X75926
- 10 F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801
- 15 F-PLACE1002450//HS\_3233\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769
- F-PLACE1002465
- 20 F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262
- 25 F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926
- 30 F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060
- F-PLACE1002499
- 35 F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927
- 40 F-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930
- F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256
- 45 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:65//AC004774
- 50 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575
- 55 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314



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F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523

5 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443

10 F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109

F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.0013:375:64//AC005537

15 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785

20 F-PLACE1002625

F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281

25 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765

30 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180

F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726

35 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723

40 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273

45 F-PLACE1002772//HS\_3058\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567

50 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259

F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927

55 F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879

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F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994

F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295

5

F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691

10

F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//9.3e-41:240:93//M27877

15

F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045

20

F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140

F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126

25

F-PLACE1002881//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200

30

F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//U19889

35

F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120

F-PLACE1002962

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F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558

45

F-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605:93//AL023755

F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP Homo sapiens genomic clone 2338I16, genomic survey sequence.//1.9e-13:100:95//AQ054760

50

F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

55

F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551

F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088

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- 5 F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829
- F-PLACE1003045//H.sapiens CpG island DNA genomic Mse1 fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200
- 10 F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158
- 15 F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875
- F-PLACE1003108
- 20 F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219
- F-PLACE1003145
- 25 F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206
- 30 F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
- 35 F-PLACE1003176//HS\_2255\_A2\_B01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934
- 40 F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:901//AC005095
- F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276
- 45 F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466
- 50 F-PLACE1003238//HS\_3239\_A2\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954
- 55 F-PLACE1003249
- F-PLACE1003256

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F-PLACE1003258//HS\_3223\_A1\_G10\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-  
07:227:65//AQ190317

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F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11,  
genomic survey sequence.//1.1e-13:97:95//AQ057429

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F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and  
9.//2.3e-92:485:95//M27877

F-PLACE1003334

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F-PLACE1003342

20

F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14  
unordered pieces.//1.0e-20:179:84//AC004951

25

F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3)  
mRNA, complete cds.//8.0e-143:773:92//U92715

F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:  
402:70//AC004095

30

F-PLACE1003366

35

F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:  
60//AL034558

F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete  
sequence.//6.0e-18:471:61//AC005247

40

F-PLACE1003375

45

F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium  
cancer, segment 10/10.//2.3e-157:779:96//AB020878

F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:  
596:91//M83680

50

F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5, genomic  
survey sequence.//0.85:140:65//AQ268588

55

F-PLACE1003420//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
clone Y1E3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388

F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:

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61//AF015470

5 F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401

F-PLACE1003493

10 F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//8.2e-41:379:78//AC002994

15 F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859

20 F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL008729

25 F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336

F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831

30 F-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297

35 F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547

40 F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688

45 F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324

50 F-PLACE1003584//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-56, complete sequence.//0.0038:465:57//AL010230

F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557

55 F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476

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F-PLACE1003596//Mus musculus integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260

5 F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200

F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356

10

F-PLACE1003611//HS\_2198\_B1\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475

15

F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226

20

F-PLACE1003625//HS\_2238\_B2\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662

25

F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478

F-PLACE1003669

30

F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830

35

F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305

40

F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920

45

F-PLACE1003723//HS\_2231\_A2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672

50

F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297

55

F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840

F-PLACE1003762

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F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014

5 F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160

10 F-PLACE1003783//HS\_2190\_A2\_C02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757

15 F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210

20 F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.015:296:60//U52112

25 F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

30 F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858//Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

35 F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

40 F-PLACE1003870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

45 F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134

F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

50 F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//D42108

55 F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone

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328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

5 F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//2.7e-86:533:87//U49385

10 F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full-length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251

15 F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505

20 F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence-//1.0:223:62//AQ239494

25 F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954

30 F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666

35 F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052

40 F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651

F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658

45 F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355

50 F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099

55 F-PLACE1004161

F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071



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F-PLACE1004197

5 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493

10 F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

15 F-PLACE1004256//HS\_2010\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434

20 F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034

F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806

25 F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121

30 F-PLACE1004274//H.sapiens CpG island DNA genomic Mse1 fragment, clone 18g6, forward read cpg18g6.ft1b.//8.6e-37:196:98//Z57691

F-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//6.0e-156:756:97//AF084830

35 F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence.//0.0060:635:57//AB011480

40 F-PLACE1004289//HS\_3023\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451

45 F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL021411

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588

50 F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 DS07968 (D117)), complete sequence.//0.87:206:59//AC004267

55 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139:688:97//AF100153

F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4.1e-81:

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498:89//AF046631

- 5 F-PLACE1004384//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653
- F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:615:62//U70855
- 10 F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027
- 15 F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//2.4e-08:129:76//AC005532
- F-PLACE1004428//R.norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188
- 20 F-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283
- 25 F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739
- 30 F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954
- 35 F-PLACE1004467//HS\_2058\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700
- 40 F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877
- 45 F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15; genomic survey sequence.//3.3e-20:140:92//B80243
- F-PLACE1004491//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709
- 50 F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150
- F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.2e-146:699:98//AF040701
- 55 F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

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F-PLACE1004518

5 F-PLACE1004548//Dictyostelium discoideum MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962

10 F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

15 F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds.//0.00013:188:67//AB001868

20 F-PLACE1004645//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//0.66:337:60//Z95120

25 F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673

F-PLACE1004658//H.sapiens CpG island DNA genomic Mse1 fragment, clone 55h1, forward read cpg55h1.ft1a./12.4e-34:188:98//Z61632

30 F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence.//1.0:148:65//Z81140

35 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561

40 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//4.3e-109:625:91//AF035606

45 F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//1.9e-152:759:96//AB020860

50 F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152

55 F-PLACE1004691//HS\_3044\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323

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- 5 F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577
- 10 F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551
- 15 F-PLACE1004722//HS\_3052\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959
- 20 F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498
- 25 F-PLACE1004740//RPCI11-58A7.TJ RPCI11 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766
- 30 F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555
- 35 F-PLACE1004751
- 40 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367
- 45 F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713
- 50 F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157
- 55 F-PLACE1004804
- F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710
- F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.8e-39:207:99//AC005921
- F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613
- F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849

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- 5 F-PLACE1004827//HS\_2230\_A2\_A05\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-  
38:330:81//AQ299313
- F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825
- 10 F-PLACE1004838//HS\_3241\_A2\_A04\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-  
87:425:98//AQ206740
- 15 F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//I92819
- F-PLACE1004868
- 20 F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No.  
9.//0.14:465:59//Z97344
- F-PLACE1004900
- 25 F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4,  
genomic survey sequence.//3.6e-06:56:100//AQ261184
- 30 F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete  
sequence.//2.6e-151:770:91//AC005058
- 35 F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:  
459:84//U97571
- F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-  
106:545:95//AF070671
- 40 F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4.  
Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete  
sequence.//3.5e-45:226:84//AL020989
- 45 F-PLACE1004937
- F-PLACE1004969
- 50 F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete  
sequence.//0.012:316:61//AC004843
- 55 F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2  
Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted  
repeat, complete sequence.//4.7e-39:394:77//AL031073

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- F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833
- 5 F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590:61//AE001373
- F-PLACE1005026
- 10 F-PLACE1005027
- F-PLACE1005046
- 15 F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867
- 20 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148
- F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//AF059569
- 25 F-PLACE1005077
- 30 F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//6.9e-29:253:77//AC004673
- F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//AC002316
- 35 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734:96//AC005225
- 40 F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//AC004476
- 45 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081
- F-PLACE1005111
- 50 F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.00051:287:63//L14320
- 55 F-PLACE1005146//HS\_3071\_A1\_E03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=5 Row=I, genomic survey sequence.//7.4e-38:299:82//AQ103361

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- 5 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//AC002451
- F-PLACE1005176
- 10 F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey sequence.//0.99:211:63//AQ054651
- F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey sequence.//2.7e-07:80:90//AQ074445
- 15 F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061
- 20 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.70:245:63//AC004965
- F-PLACE1005243
- 25 F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812
- 30 F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4\_2g).//9.6e-33:177:98//Z70695
- F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182
- 35 F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183
- 40 F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//M25757
- F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621
- 45 F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167
- 50 F-PLACE1005327//HS\_3080\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116
- 55 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//AC004794

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F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237:92//AC000380

5 F-PLACE1005373

F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//AF017104

10

F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991

15 F-PLACE1005453//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854

F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859

20

F-PLACE1005471//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581

25

F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191

30 F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878

35

F-PLACE1005481//RPC11-74L17.TJ RPC11 Homo sapiens genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885

40 F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//2.1e-67:325:99//AF080394

45 F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//0.015:403:61//AC005589

F-PLACE1005526//H.sapiens CpG island DNA genomic MseI fragment, clone 9f1, reverse read cpg9f1.rt1a.//3.6e-27:159:96//Z66485

50

F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038

55 F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence.//6.5e-18:234:72//AC004860



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F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence.//1.2e-14:123:75//AL025925

5 F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//0.43:209:66//X02354

10 F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//9.3e-113:536:97//AC004707

15 F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59//AC005504

F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds.//0.00056:289:63//AB014517

20 F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//1.2e-111:262:89//AC004126

25 F-PLACE1005603

F-PLACE1005611//F16O5TFC IGF Arabidopsis thaliana genomic clone F16O5, genomic survey sequence.//2.0e-10:209:66//B98589

30 F-PLACE1005623

35 F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840

40 F-PLACE1005639//HS\_3095\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022

F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255

45 F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase.//1.3e-51:480:74//X59618

50 F-PLACE1005666//RPCI11-78O15.TV RPCI11 Homo sapiens genomic clone R-78O15, genomic survey sequence.//8.7e-05:243:62//AQ284667

55 F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457

F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422

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- 5 F-PLACE1005730//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-  
24:286:74//AQ231147
- 10 F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-  
55:621:71//U15635
- 15 F-PLACE1005755//HS\_2213\_A2\_H11\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2213 Col=22 Row=O, genomic survey sequence.//1.4e-  
25:290:75//AQ136844
- 20 F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH),  
complete cds.//4.5e-40:297:70//M16200
- 25 F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:  
287:63//Y12517
- 30 F-PLACE10058021//Homo sapiens PAC clone DJ044L15 from Xq23, complete  
sequence.//5.0e-109:530:98//AC004827
- 35 F-PLACE1005803//HS\_3092\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence.//2.4e-  
08:76:96//AQ103695
- 40 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.4e-  
126:636:96//AF027156
- 45 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//2.6e-154:  
739:98//AF065482
- 50 F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING  
DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150
- 55 F-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
contig 4-105, complete sequence.//0.00080:663:58//AL010283
- F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//AC004153
- F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-  
36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//1.8e-  
46:278:85//AL031432
- F-PLACE1005851

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F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//5.0e-120:701:89//X75931

5 F-PLACE1005884//CIT-HSP-2333O12.TR CIT-HSP Homo sapiens genomic clone 2333O12, genomic survey sequence.//4.6e-78:385:98//AQ039226

10 F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds.//9.3e-16:638:57//U29892

15 F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds.//1.0:178:65//U67136

F-PLACE1005921//M.musculus mRNA for immunity associated protein 38.//6.6e-17:614:59//Y08026

20 F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151

25 F-PLACE1005925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405

F-PLACE1005932

30 F-PLACE1005934//H.sapiens CpG island DNA genomic Mse1 fragment, clone 165g2, forward read cpg165g2.ft1a.//8.3e-43:247:93//Z57153

35 F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719

40 F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236

45 F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081

F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070

50 F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925

F-PLACE1005968

55 F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866

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F-PLACE1006002//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090

5 F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442

10 F-PLACE1006011//Mus musculus poly-(ADPribose)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521

15 F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 -complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299

F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139

20 F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906

25 F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200

30 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023

F-PLACE1006129

35 F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597

40 F-PLACE1006143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015

45 F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2.//0.048:290:60//D85750

F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-1054O2 map 10q25, complete sequence.//3.2e-129:466:96//AC005661

50 F-PLACE1006164//HS\_3003\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388:93//AQ118200

55 F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385:86//AC005239

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F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972

5 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694:99//AF091433

10 F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283:70//AC003658

F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//2.2e-94:648:84//L25125

15 F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:58//U75931

20 F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175:64//B19803

F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence.//2.1e-19:149:90//AQ039880

25 F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.51:290:58//U91327

30 F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142

35 F-PLACE1006246//RPCI11-36I23.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence.//2.6e-31:176:97//AQ045400

F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548

40 F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447

45 F-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320

F-PLACE1006318

50 F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454

55 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721

F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic

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sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504

5 F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559

F-PLACE1006368//X.laevis mRNA for KLP2 protein.//3.0e-25:376:68//X94082

10 F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711:97//AC004232

F-PLACE1006382

15

F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-110:539:97//AF062085

20 F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029

25 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735

F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129

30

F-PLACE1006445//HS\_3071\_A1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ 103347

35

F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496

40 F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250:59//Z15118

F-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977

45

F-PLACE1006488//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68) .//6.5e-86:478:91//X53744

50 F-PLACE1006492

F-PLACE1006506

55 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083

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F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355

5 F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510

F-PLACE1006540

10

F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998

15 F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044

20 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670

F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//0.98:514:59//AC004470

25

F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589

30 F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015

35 F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276

F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688

40

F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790

45 F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:380:62//U67916

50 F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.//1.5e-78:520:86//Z98048

55 F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequencer/1.9e-135:378:99//AC005626

F-PLACE1006760//CIT-HSP-2336O13.TR CIT-HSP Homo sapiens genomic clone 2336O13,

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genomic survey sequence.//0.018:147:66//AQ039246

5 F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426

10 F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487

15 F-PLACE1006792//HS\_3165\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559

F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513

20 F-PLACE1006800//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272

25 F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init. region.//9.1e-09:369:62//K00915

30 F-PLACE1006815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033

F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230

35 F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350

40 F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559

45 F-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378

F-PLACE1006878

50 F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//1.0:236:62//Z95120

55 F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672

F-PLACE1006904



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F-PLACE1006917//H.sapiens CpG island DNA genomic Mse1 fragment, clone 79g10, forward read cpg79g10.ft1a.//1.3e-21:131:98//Z63175

5 F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063

10 F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308

F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447

15 F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//U23921

20 F-PLACE1006961//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.6e-06:651:58//AJ223323

F-PLACE1006962//H.sapiens ir1B mRNA.//7.1e-15:202:71//X63417

25 F-PLACE1006966//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594

30 F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188

35 F-PLACE1007014//Rattus norvegicus equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305

F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403; complete sequence.//5.1e-17:285:70//AC005777

40 F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat\*.//6.2e-131:775:89//Z82899

45 F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895

50 F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.3e-131:652:97//AC005224

55 F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368

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- F-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//4.1e-124:687:91//U72194
- 5 F-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139
- 10 F-PLACE1007112//HS\_2234\_B2\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801
- 15 F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112
- 20 F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt].//4.9e-15:386:62//S68151
- F-PLACE1007178//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140
- 25 F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899
- F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//2.8e-08:269:63//S74494
- 30 F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:405:87//D50495
- 35 F-PLACE1007242//HS\_3006\_A1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443
- 40 F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082
- 45 F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908
- F-PLACE1007274//HS\_3003\_A1\_D08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154
- 50 F-PLACE1007276//Fugu rubripes GSS sequence, clone 014O10aG11, genomic survey sequence.//0.0052:228:62//AL024982
- 55 F-PLACE1007282//F.rubripes GSS sequence, clone 019O07aB3, genomic survey sequence.//0.024:289:58//AL011743

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F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:69//AC002492

5 F-PLACE1007301//Dictyostelium discoideum gene for TRFA, complete cds.//0.069:761:57//AB009080

F-PLACE1007317

10

F-PLACE1007342

15 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:567:98//AF096870

F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-59:613:75//AC005077

20

F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:70//U88167

F-PLACE1007386

25

F-PLACE1007402//HS\_2170\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162:67//AQ125590

30

F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:93//AF093772

35

F-PLACE1007416

F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973

40

F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1e-17:374:64//AF041433

45

F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:317:93//L40391

F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//0.0019:280:64//AL031117

50

F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence, complete sequence.//2.5e-24:362:71//AC002302

55

F-PLACE1007484

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F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds.//3.8e-14:293:63//AF017370

5 F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//4.6e-10:152:75//AL031311

10 F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//3.6e-139:477:98//AC004231

15 F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.//0.0055:395:59//AF015461

20 F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S rRNA gene.//0.0013:550:58//U11682 F-PLACE1007537//H.sapiens CpG island DNA genomic Mse1 fragment, clone 198g6, reverse read cpg198g6.rt1a.//0.98:121:67//Z60280

25 F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508

30 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds.//3.1e-69:733:71//AB014561

F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.022:393:61//X03240

35 F-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565:97//AL031665

40 F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey sequence.//2.0e-22:304:70//AQ111183

45 F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.0:386:59//AC005245

F-PLACE1007621

50 F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-88:276:96//AC006064

F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79//M26132

55 F-PLACE1007649

F-PLACE1007677//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone

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968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567:64//AL023755

F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:287:66//X15120

5

F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122:70//U23452

F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//0.85:117:71//L40483

10

F-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75:88//AL031662

15

F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-147:709:97//AF061243

20

F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence.//1.0:510:58//AB005231

F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516:89//U86698

25

F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585

30

F-PLACE1007737//Homo sapiens clone DJ0847O08, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.8e-22:806:60//AC005484

35

F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504

F-PLACE1007746//HS\_2268\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780

40

F-PLACE1007791//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.63:241:58//AL031749

45

F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879\_D\_6, complete sequence.//1.0e-120:743:87//AC005273

50

F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658

55

F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438

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- F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903
- 5 F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP000010
- F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174
- 10 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309
- 15 F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271
- F-PLACE1007877
- 20 F-PLACE1007897
- F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//AB007956
- 25 F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097
- 30 F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//AC006157
- 35 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//AF084530
- 40 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:730:98//AF079529
- F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//U13262
- 45 F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758
- 50 F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695
- F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-163:786:98//AC005628
- 55 F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:84//L31840

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- 5 F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719
- 5 F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883
- 10 F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883
- 15 F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//7.5e-06:414:60//AF069163
- 20 F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867
- 25 F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase Ix genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586
- 30 F-PLACE1008132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199
- 35 F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849
- 40 F-PLACE1008181//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397
- 45 F-PLACE1008198//HS\_3073\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450
- 50 F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-162:791:97//AC005069
- 55 F-PLACE1008209
- 55 F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332
- 55 F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence.//6.7e-28:165:95//AQ039317
- 55 F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987

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F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M29123

5 F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.011:96:73//AC005913

10 F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672:77//AF078779

15 F-PLACE1008329//HS\_2027\_A1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence.//8.7e-09:116:81//AQ244432

F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176

20 F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-27:157:78//AC005000

25 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659:98//AB014579

30 F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence.//7.1e-08:398:60//AQ016352

35 F-PLACE1008369//HS\_2251\_B1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217:93//AQ066512

F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.4e-11:403:64//AC005856

40 F-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417

45 F-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:96//AC004604

50 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326

F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688

55 F-PLACE1008424

F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of



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hepatocellular colorectal and non-small cell lung cancer , segment 7/11.//1.0e-88:331:84//AB020864

- 5 F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317
- 10 F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479
- 15 F-PLACE1008455//HS\_2064\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589
- 20 F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526
- 25 F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014
- 30 F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494
- 35 F-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778
- 40 F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555
- 45 F-PLACE1008532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097
- 50 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997
- 55 F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571
- F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//U73023
- F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334
- F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.9e-09:198:71//AC005077

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F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence.//0.68:568:59//AC005373

5 F-PLACE1008626//HS\_3221\_A2\_F03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147:82//AQ180967

10 F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586:88//Y12836

F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence.//0.00085:203:66//B53732

15 F-PLACE1008630//Sequence 26 from Patent WO9517522.//9.7e-05:97:80//A45356

20 F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23 :299:64//D38595

25 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622:99//AF044333

F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89:76//AQ060732

30 F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420:97//AF038406

35 F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349:98//AQ007199

40 F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.14:347:59//AC004260

45 F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//7.9e-25 :244:71//AC003037

F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//4.5e-120:503:97//AF060543

50 F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370:61//AF001549

55 F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence.//3.3e-08:220:65//AQ036643

F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete

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cds.//1.7e-120:470:97//AF030933

5 F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:504:89//AF032668

10 F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212:74//AL021920

F-PLACE1008854

15 F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//4.7e-77:477:84//Z82209

20 F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699:70//AC005539

25 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:164:68//M63660

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6.4e-158:753:98//AB018308

30 F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:400:63//AC002042

35 F-PLACE1008934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022312

40 F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds.//4.3e-41:282:87//L15309

F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences.//5.9e-15:710:60//M34651

45 F-PLACE1009020//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//1.9e-21:167:86//AQ253727

50 F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117

55 F-PLACE1009039//HS\_2034\_A2\_F08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence.//0.17:252:59//AQ230137

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- 5 F-PLACE1009045//HS\_3185\_B2\_B03\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence.//1.9e-  
34:260:86//AQ172861
- 10 F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5'flank and exon  
1.//4.7e-70:463:80//D00766
- F-PLACE1009050//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer  
Institute Human PAC library) complete sequence.//0.63:280:61//AC004241
- 15 F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete  
CDS.//5.9e-113:725:85//AJ005073
- 20 F-PLACE1009090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021919
- F-PLACE1009091//Homo sapiens clone DJ096816, complete sequence.//0.027:630:  
58//AC006016
- 25 F-PLACE1009094
- F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds.//2.1e-85:726:  
76//M36515
- 30 F-PLACE1009110
- 35 F-PLACE1009111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752
- 40 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3)  
mRNA, complete cds.//3.4e-138:671:97//AF035586
- F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-23:718:  
59//D25215
- 45 F-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT  
SEQUENCE.//6.1e-142:684:98//AJ011929
- 50 F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28,  
WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AP000031
- 55 F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3'region involved in DNA  
excision repair.//1.0:173:60//X52222
- F-PLACE1009166

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- 5 F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//4.0e-35:257:85//AC002070
- F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//2.9e-19:288:72//AC004805
- 10 F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence.//0.053:388:60//AB008266
- 15 F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds.//1.8e-50:317:89//AF061242
- F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5, genomic survey sequence.//0.91:114:67//AQ281881
- 20 F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198
- 25 F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein.//1.1e-106:495:88//X63203
- 30 F-PLACE1009246//HS\_3058\_B1\_A06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence.//0.10:175:68//AQ185945
- 35 F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.8e-94:575:89//U47024
- 40 F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.//0.0017:350:62//U23862
- F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds.//3.0e-06:411:59//U83192
- 45 F-PLACE1009328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034399
- 50 F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain.//0.071:253:62//D87015
- F-PLACE1009338//RPCI11-74N24 TV RPCI11 Homo sapiens genomic clone R-74N24, genomic survey sequence.//2.4e-34:180:100//AQ268811
- 55 F-PLACE1009368

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F-PLACE1009375

5 F-PLACE1009388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022311

10 F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds.//4.3e-78:730:  
74//M27878

F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt].//0.16:95:71//S71494

15 F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete  
sequence.//1.6e-150:701:99//AC005919

20 F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence.//2.9e-73:442:  
88//AF046700

F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment  
148/162.//0.012:582:56//AL022022

25 F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA,  
complete cds.//4.6e-21:146:93//AF012872

30 F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence.//2.9e-31:264:  
81//AF046660

F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84//I30536

35 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete  
sequence.//1.9e-142:704:97//AC004531

40 F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence.//2.2e-09:  
235:68//AC004601

45 F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete  
sequence.//2.9e-83:171:92//U91321

50 F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-  
13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF  
exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein.  
Contains ESTs, STSs and GSSs, complete sequence.//3.8e-69:175:92//Z94160

55 F-PLACE1009539//Mus musculus synaptojanin 2 isoform alpha mRNA, complete cds.//7.0e-  
26:237:78//AF041862

F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-  
13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to

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monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//AL031587

5 F-PLACE1009571//RPCI11-60K12.TK RPCI11 Homo sapiens genomic clone R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869

F-PLACE1009581

10

F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence.//6.6e-19:309:70//AC003959

15 F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-09:485:59//AF016049

20 F-PLACE1009607//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824

F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC004157

25

F-PLACE1009621

30 F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey sequence.//2.7e-15:100:98//B33248

35 F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC005308

F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL021816

40 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.4e-171:816:98//AB011159

45 F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.4e-67:437:87//AC005177

F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:701:98//AF062534

50

F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-98:228:100//AC006011

55 F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//2.2e-130:736:91//AC000109

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F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1e-13:311:64//Y08026

5 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2e-125:602:98//AF046024

F-PLACE1009794

10

F-PLACE1009798//Hnman DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.3e-73:271:84//AL030996

15

20 F-PLACE1009845

F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end.//0.00023:147:65//M64620

25 F-PLACE1009879//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397

30 F-PLACE1009886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427

F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//0.0044:232:60//AQ251431

35

F-PLACE1009908//S.pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369

40 F-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//5.9e-48:304:87//M63005

F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529

45

F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066

50 F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//I25655

F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026

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F-PLACE1009971



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F-PLACE1009992//HS\_3178\_B1\_F04\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-  
23:142:95//AQ150311

5

F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:  
231:64//Z81029

10

F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete  
cds.//7.9e-87:552:80//U48288

F-PLACE1010023

15

F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3.  
Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to  
(predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the  
KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-  
101:181:98//AL031775

20

F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:  
95//X84692

25

F-PLACE1010069//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114

30

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:  
792:98//AF065482

35

F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:  
77//D25540

40

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:  
98//AB007925

F-PLACE1010089//HS\_3111\_A1\_E08\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3111 Col=15 Row=I, genomic survey sequence.//4.8e-  
07:124:78//AQ101268

45

F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85//X64411

50

F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic  
sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506

55

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.8e-  
25:728:60//AF059569

F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//6.5e-

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25:488:63//Z93928

- 5 F-PLACE1010134//S.pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164
- F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83 :409:98//AJ222636
- 10 F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence.//1.5e-28:163:98//AQ196757
- F-PLACE1010181//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//2.4e-15:197:72//AC004973
- 15 F-PLACE1010194//Ictalurus punctatus tumor supressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967
- 20 F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829
- F-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377
- 25 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917
- 30 F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence; WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710
- F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00040:231:64//Z81029
- 35 F-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464
- 40 F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-1 0:185:67//AL031005
- 45 F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468
- 50 F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837
- 55 F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome.//2.8e-08:384:64//L06178
- F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo

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sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252

- 5 F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.//0.94:398:57//AL022121
- 10 F-PLACE1010364//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985
- 15 F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//0.066:88:76//AC004675
- F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825
- 20 F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927
- 25 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081
- F-PLACE1010492
- 30 F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//J82695
- F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145 :684:98//AR016417
- 35 F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677
- 40 F-PLACE1010562//RPC11-65I16.TK RPC11 Homo sapiens genomic clone R-65I16, genomic survey sequence.//0.017:216:67//AQ200831
- 45 F-PLACE1010579//Homo sapiens full-length insert cDNA Y123D12.//3.9e-19:147:89//AF075014
- F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125
- 50 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186
- 55 F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308
- F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:

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60//AL034558

- 5 F-PLACE1010624//*Streptomyces coelicolor* cosmid 5A7.//1.4e-05:518:61//AL031107
- F-PLACE1010628//*Homo sapiens* clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846
- 10 F-PLACE1010629//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682
- 15 F-PLACE1010630//*Arabidopsis thaliana* genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872
- F-PLACE1010631//*Homo sapiens* clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069
- 20 F-PLACE1010661
- F-PLACE1010662//*Arabidopsis thaliana* DNA chromosome 4, BAC clone F7J7 (ESSA project) //0.90:257:61//AL021960
- 25 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376
- 30 F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583
- 35 F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678
- F-PLACE1010739//HS\_2013\_B2\_B10\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864
- 40 F-PLACE1010743//*R.norvegicus* mRNA for myr5.//1.7e-87:582:85//X77609
- 45 F-PLACE1010761//*Homo sapiens* chromosome 17, clone hRPK.294\_J\_22, complete sequence.//4.7e-45:235:99//AC005921
- 50 F-PLACE1010771//*M.musculus* HCNGP mRNA.//1.6e-135:801:88//X68061
- F-PLACE1010786//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-15, complete sequence.//0.35:334:60//AL010221
- 55 F-PLACE1010800//RPC11-79H17.TV RPC11 *Homo sapiens* genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252

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F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384

5 F-PLACE1010811//RPC111-51N5.TK RPC111 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380

10 F-PLACE1010833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283

F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229

15 F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.4e-94:422:95//AB020868

20 F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530:90//Z67747

F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182

25 F-PLACE1010891

30 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-26:394:68//AC003997

F-PLACE1010900

35 F-PLACE1010916//HS\_2242\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687

40 F-PLACE1010917

F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688

45 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126

50 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds.//5.6e-90:437:98//AF064243

55 F-PLACE1010944//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247

F-PLACE1010947

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- 5 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey sequence.//2.1e-29:190:91//B98965
- F-PLACE1010960//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//0.00074:421:60//AL010226
- 10 F-PLACE1010965//CIT-HSP-2386K24:TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey sequence.//1.8e-84:412:99//AQ240696
- 15 F-PLACE1011026//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.00037:257:64//AL008972
- 20 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence.//3.8e-06:315:65//AC005348
- F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669
- 25 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636
- F-PLACE1011054//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 981L23, WORKING DRAFT SEQUENCE.//3.8e-27:196:84//AL031686
- 30 F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049
- 35 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:100//S75548
- 40 F-PLACE1011090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//5.1e-80:479:89//AL031687
- F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//2.3e-24:192:84//L14684
- 45 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249
- 50 F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//0.010:345:60//B19698
- 55 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00013:95:76//AQ109305
- F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete

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sequence.//3.7e-111:692:87//AC004893

- 5 F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-31:194:92//M84443
- 10 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence.//3.1e-43:447:72//AC002288
- F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//3.3e-124:584:99//AF038664
- 15 F-PLACE1011214//HS\_2046\_A2\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965
- 20 F-PLACE1011219
- F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey sequence.//2.4e-20:119:100//AQ279801
- 25 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101
- 30 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//AC005014
- 35 F-PLACE1011273//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y37D8, WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819
- 40 F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66:98//B81770
- F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647
- 45 F-PLACE1011310//H.sapiens CpG island DNA genomic Mse1 fragment, clone 53c10, reverse read cpg53c10.rt1b.//1.4e-05:57:100//Z61496
- 50 F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290
- 55 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265
- F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388\_F\_14, complete sequence.//2.4e-38:186:83//AC005375

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- 5 F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:  
689:63//AF023919
- F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310
- 10 F-PLACE1011399//paramecium species 7,325 mt dna dimer: replication init.  
region.//0.00011:255:63//K00919
- F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:  
62//AJ006996
- 15 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:  
98//AB011102
- 20 F-PLACE1011452//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT  
SEQUENCE.//1.1e-53:557:73//AJ011929
- F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7,  
25 complete sequence.//3.5e-71:498:80//AC004605
- F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:  
99//AB018255
- 30 F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:  
675:99//AF065482
- 35 F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:  
59//J00964
- F-PLACE1011503
- 40 F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:  
99//AC004968
- 45 F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941  
bp).//0.00036:296:61//X83546
- F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete  
50 sequence.//1.1e-38:315:82//AC004984
- F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA,  
complete cds.//1.3e-65:268:86//AF054180
- 55 F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete  
sequence.//2.0e-82:188:96//AC004477



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- 5 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.8e-153:752:97//AC005224
- 10 F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660
- 15 F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729
- 20 F-PLACE1011646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383
- F-PLACE1011649
- F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062
- F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374
- 25 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507
- 30 F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719
- 35 F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487
- F-PLACE1011725
- 40 F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737
- 45 F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157
- 50 F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003
- F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944
- 55 F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330

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- F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147
- 5 F-PLACE1011874//Homo Sapiens Chromosome X clone bW XD312, complete sequence.//2.5e-141:678:98//AC004478
- 10 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152
- 15 F-PLACE1011891//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392
- 20 F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969
- F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400
- 25 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617
- 30 F-PLACE1011962//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369
- 35 F-PLACE1011964//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799
- 40 F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529
- 45 F-PLACE1011995//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054
- F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256
- 50 F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//1.7e-62:293:88//AC005837
- 55 F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057
- F-PLACE2000007
- F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete

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sequence.//5.2e-102:489:99//AC005578

5 F-PLACE2000014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574

10 F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069

15 F-PLACE2000017//HS\_3042\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074

20 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556

25 F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638

30 F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913

35 F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//AF041082

40 F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505

45 F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626

50 F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//AC003101

55 F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010

F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457

F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219

F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910

F-PLACE2000100//HS\_3184\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D

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Homo sapiens genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004

5 F-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848

10 F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491

F-PLACE2000115

15 F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//6.2e-43:362:80//AC004531

20 F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F15, genomic survey sequence.//5.4e-35:206:94//AQ284166

F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814:59//AC002070

25 F-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//3.6e-165:799:97//AL020995

30 F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701

F-PLACE2000170

35 F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552:88//AC006005

40 F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//0.98:201:64//AC004032

F-PLACE2000187

45 F-PLACE2000216

F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence.//0.00039:325:58/B75888

50 F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237:78//AC003003

55 F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//2.4e-92:236:94//AC005902

F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31

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Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331:78//AL031577

5 F-PLACE2000274//Anthocidaris crassispina mRNA for B2HC, partial cds.//8.5e-48:765:66//AB012308

10 F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//8.3e-08:662:58//US2064

15 F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-08:95:81//AC006021

20 F-PLACE2000317//HS\_3183\_B2\_F05\_MR CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346:99//AQ172747

F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-14:402:65//AC004952

25 F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.//4.5e-77:555:82//AF026554

30 F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//1.8e-14:259:71//U66829

35 F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//6.0e-34:376:74//AC003006

40 F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence.//8.4e-21:288:69//AQ013849

F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence.//5.0e-114:692:80//U49973

45 F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.38:356:58//AC005182

50 F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence.//0.064:132:68//AQ051776

55 F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.6e-130:776:88//AC003658

F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808:83//AC005909

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- 5 F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila  
'period' gene.//0.87:286:63//X06967
- F-PLACE2000399
- 10 F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2.9e-59:532:  
68//Z36238
- F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog  
mRNA, complete cds.//0.44:553:56//U89984
- 15 F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303:  
86//M13792
- 20 F-PLACE2000425//HS\_3047\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3047 Col=9 Row=O, genomic survey sequence.//2.8e-  
42:224:97//AQ126949
- 25 F-PLACE2000427
- F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete  
sequence.//1.1e-19:363:67//AC005821
- 30 F-PLACE2000435//HS\_3036\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-  
06:184:66//AQ096999
- 35 F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:  
550:62//AL021492
- 40 F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete  
sequence.//1.0e-78:604:80//AC006025
- 45 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10,  
complete sequence.//8.2e-05:330:63//AC002300
- F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154),  
complete sequence.//5.7e-168:816:97//AC005740
- 50 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and  
cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037
- 55 F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11  
unordered pieces.//3.4e-59:598:74//AC005057

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F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602

5 F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187

F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075

10

F-PLACE3000029

15 F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267

F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-17:250:74//AC005368

20

F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006

25 F-PLACE3000119//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670

30 F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668

F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//1.8e-48:330:79//AC005695

35

F-PLACE3000136

40 F-PLACE3000142//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520

F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662

45 F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053

50 F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474

55 F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//7.4e-173:822:98//AC005277

F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133,

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R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682

F-PLACE3000157

5

F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500

F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7,  
genomic survey sequence.//0.080:259:59//B50878

10

F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete  
sequence.//9.8e-158:749:98//AC006130

15

F-PLACE3000194

F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey  
sequence.//1.4e-08:164:68//AL003352

20

F-PLACE3000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207

25

F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete  
sequence.//6.6e-21:312:67//AC005013

30

F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67)  
collagen type VII intergenic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982

F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered  
pieces.//9.3e-43:383:79//AC004086

35

F-PLACE3000220//RPC11-54B4.TV RPC11 Homo sapiens genomic clone R-54B4,  
genomic survey sequence.//2.4e-36:381:76//AQ082056

40

F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6  
unordered pieces//7.2e-135:721:91//AC005231

45

F-PLACE3000226

F-PLACE3000230//Homo sapiens c1cr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6)  
genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete  
sequence.//3.3e-80:498:78//U95626

50

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4.  
Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced  
Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,  
6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032,  
complete sequence.//2.6e-54:254:92//Z98046

55



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- F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169
- 5 F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424
- F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//1.8e-21:350:68//AF001548
- 10 F-PLACE3000276//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147
- 15 F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//AC005328
- 20 F-PLACE3000310
- F-PLACE3000320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379
- 25 F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//3.3e-35:419:68//AC005822
- 30 F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence.//2.7e-20:119:99//AQ061543
- 35 F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642
- 40 F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:98//AC006055
- F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds.//2.3e-107:592:92//AF084205
- 45 F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//2.1e-37:480:70//Z83732
- 50 F-PLACE3000353
- F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.00011:373:60//AC005969
- 55 F-PLACE3000363

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F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007

5 F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545

10 F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154

15 F-PLACE3000399//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630

20 F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239

25 F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25 :292:73//AC006023

F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence.//1.1e-10:154:74//AQ008761

30 F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.9e-41:515:72//AC005701

35 F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443

40 F-PLACE3000413

F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//0.0018:664:55//B11305

45 F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719

50 F-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.6e-146:732:96//AL031284

55 F-PLACE3000475//HS\_2164\_A2\_H10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=O, genomic survey sequence.//1.5e-07:159:71//AQ132983

F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains

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ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//2.9e-11:213:70//Z83843

- 5 F-PLACE4000009//Sequence 93 from patent US 5616500.//9.9e-08 :692:60//I39845
- F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1.1e-116:331:100//AB018352
- 10 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.0e-05:244:63//AC004131
- 15 F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926
- F-PLACE4000052//M.musculus abcl mRNA.//1.5e-110:671:88//X75926
- 20 F-PLACE4000063
- F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation.//3.7e-12:114:85//X74311
- 25 F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence.//0.11:245:60//AQ108342
- 30 F-PLACE4000100//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848
- 35 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1.2e-145:684:99//AB007931
- F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234
- 40 F-PLACE4000129
- 45 F-PLACE4000131//HS\_3139\_B2\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207
- 50 F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622
- 55 F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U09367
- F-PLACE4000192

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F-PLACE4000211

5 F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01,  
genomic survey sequence.//1.2e-14:177:76//B17158

10 F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//9.8e-116:662:  
89//AF030430

15 F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete  
sequence.//5.2e-54:363:70//AC003973

F-PLACE4000247

20 F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems  
Human BAC library) complete sequence.//0.0053:229:65//AC004673

F-PLACE4000252

25 F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.0e-25:191:  
87//Z70200

30 F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete  
cds.//2.6e-23:314:71//AF084259

35 F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//5.5e-122:734:  
88//AF032667

F-PLACE4000270

F-PLACE4000300

40 F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete  
cds.//1.4e-21:135:96//L34075

45 F-PLACE4000323//HS\_2165\_B1\_B02\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-  
08:170:71//AQ125036

50 F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone  
Mu2.//2.8e-06:311:63//M10296

55 F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete  
sequence.//0.014:252:60//AE001401

F-PLACE4000367

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F-PLACE4000369

5 F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9,  
genomic survey sequence.//9.2e-46:282:86//AQ062661

10 F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11,  
genomic survey sequence.//0.96:102:70//AQ080649

15 F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:  
68//AF054088

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:  
71//AB014540

20 F-PLACE4000411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984

25 F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:  
92//Z70200

30 F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo  
sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:  
100//B41346

F-PLACE4000450

35 F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete  
sequence.//2.3e-07:273:65//AC005065

40 F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete  
sequence.//4.1e-34:351:70//AC005821

45 F-PLACE4000489//HS\_3012\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-  
36:220:92//AQ095537

50 F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer  
Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865

F-PLACE4000521//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT  
SEQUENCE.//1.6e-163:770:98//AJ011929

55 F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial  
cds.//4.0e-124:686:90//U47645

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F-PLACE4000548

F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747

5

F-PLACE4000581

F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequence.//3.6e-20:747:59//AC004474

10

F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418

15

F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281

20

F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039

F-PLACE4000650

25

F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267

30

F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816

F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577

35

F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554

40

F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616

45

F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797

F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561

50

F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637

55

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F-THYRO1000034//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353

5 F-THYRO1000035//Human Chromosome X clone bW XD187, complete sequence.//1.2e-39:303:83//AC004383

F-THYRO1000040

10

F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383

15 F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557

F-THYRO1000085

20

F-THYRO1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606

25 F-THYRO1000107

F-THYRO1000111//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403

30

F-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055

35 F-THYRO1000124//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724

40 F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142

F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096

45

F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574

50

F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331

55 F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419

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F-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207

- 5 F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214
- F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//0.38:184:64//AC005746
- 10 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698
- 15 F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552
- F-THYRO1000206//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134
- 20 F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157
- 25 F-THYRO1000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186
- 30 F-THYRO1000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156
- F-THYRO1000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055
- 35 F-THYRO1000270
- 40 F-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664
- F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068
- 45 F-THYRO1000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894
- 50 F-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233
- 55 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333



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F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//J29091

5 F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080

10 F-THYRO1000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668

F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019

15 F-THYRO1000394//HS\_2061\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672

20 F-THYRO1000395//Drosophila melanogaster ring canel protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483

25 F-THYRO1000401 3.2e-116:504:80//AF051908

F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308

30 F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573

35 F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229

40 F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196

F-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740

45 F-THYRO1000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

50 F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056

55 F-THYRO 1000505

F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563

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- 5 F-THYRO1000569//HS\_2178\_B2\_E03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499
- F-THYRO1000570
- 10 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587
- 15 F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323
- 20 F-THYRO1000602//HS\_3037\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057
- 25 F-THYRO1000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777
- F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546
- 30 F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474
- 35 F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559
- 40 F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//1.1e-68:468:84//AC005696
- 45 F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874
- F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437
- 50 F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778
- 55 F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317
- F-THYRO1000699//RPC11-50D4.TK RPC11 Homo sapiens genomic clone R-50D4,

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genomic survey sequence.//2.7e-09:135:78//AQ052641

5 F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053

10 F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320

15 F-THYRO1000734//HS\_3233\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143

F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871

20 F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523

25 F-THYRO1000777//S.griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763

F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373

30 F-THYRO1000787//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986

35 F-THYRO1000793

F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422

40 F-THYRO1000805//Homo sapiens Xp21 PAC RPC11-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468

45 F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914

50 F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053

F-THYRO1000843

55 F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782

F-THYRO1000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA,

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complete cds.//0.038:208:64//AF008573

5 F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete  
sequence.//1.9e-30:286:74//AC005477

10 F-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720

F-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//3.6e-78:432:93//AC006015

15 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA,  
partial cds.//9.2e-178:839:98//AF079529

20 F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:  
759:63//M77836

F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT  
SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229

25 F-THYRO1000952

30 F-THYRO1000974//HS\_3238\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//12.4e-  
26:154:96//AQ219846

35 F-THYRO1000975//Plasmodium falciparum Topoll gene.//0.32:491:58//X79345

F-THYRO1000983//Mwvf9A3 exon amplification products from BACs in Mwvf region Mus  
musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457

40 F-THYRO1000984//CIT-HSP-2167O17.TR CIT-HSP Homo sapiens genomic clone 2167O17,  
genomic survey sequence.//0.00015:186:66//B91313

45 F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human  
ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered  
pieces.//0.024:267:63//AC004588

50 F-THYRO1001003

F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete  
sequence.//1.1e-55:543:72//AC003695

55 F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328  
(section 5 of 148) of the complete genome.//0.94:445:58//AE000799

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F-THYRO1001062//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320

5 F-THYRO1001093//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//4.9e-34:353:76//AC006241

10 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end.//1.1e-72:742:74//L14787

F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522

15 F-THYRO1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 671O14, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595

20 F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996

25 F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486

F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178

30 F-THYRO1001173

F-THYRO1001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//J29953

35 F-THYRO1001189//HS\_3171\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330

40 F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925

45 F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300

F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036

50 F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496

55 F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.119.6e-49:586:69//AL021086

F-THYRO1001290//HS\_2045\_B1\_H09\_MR CIT Approved Human Genomic Sperm Library D

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Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237

- 5 F-THYRO1001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693
- 10 F-THYRO1001320//Homo sapiens Chromosome 22q11.2 PAC Clone p\_n5 In BCRL2-GGT Region, complete sequence.//1.1e-88:672:82//AC002472
- 15 F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114
- 20 F-THYRO1001322//HS\_3205\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025
- 25 F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288
- 30 F-THYRO1001363//Homo sapiens PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905
- 35 F-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map-10q25, complete sequence.//7.6e-168:821:97//AC005660
- 40 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607
- 45 F-THYRO1001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239
- 50 F-THYRO1001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845
- 55 F-THYRO1001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852
- F-THYRO1001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.//1.0e-91:631:82//AF064635
- F-THYRO1001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126
- F-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553

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F-THYRO1001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.0:98:70//AC000384

5 F-THYRO1001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265

10 F-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-42:357:80//AC006001

F-THYRO1001487//H.sapiens DNA sequence.//0.92:160:64//Z22449

15 F-THYRO1001534//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666

20 F-THYRO1001537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687

25 F-THYRO1001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:77//Z96074

F-THYRO1001559//Rattus norvegicus simple sequence repeat D18Mco6.//1.6e-09:351:63//AF006056

30 F-THYRO1001570//RPCI11-49B23.TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey sequence.//1.4e-65:384:91//AQ052105

35 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572

40 F-THYRO1001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808

45 F-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.786\_O\_4, complete sequence.//2.9e-26:393:68//AC005863

50 F-THYRO1001605//Dictyostelium discoideum filopodin (talA) gene, complete cds.//0.0012:436:58//U14576

55 F-THYRO1001617//Homo sapiens full-length insert cDNA clone ZD69D05.//8.6e-43:342:82//AF086381

F-THYRO1001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//6.2e-15:318:66//AC004950

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- 5 F-THYRO1001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827
- F-THYRO1001661
- 10 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//AJ225089
- F-THYRO1001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071
- 15 F-THYRO1001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857
- F-THYRO1001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745
- 20 F-THYRO1001721//, complete sequence.//9.9e-134:770:91//AC005500
- 25 F-THYRO1001738//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327
- F-THYRO1001745
- 30 F-THYRO1001746
- F-THYRO1001772//HS\_3069\_B1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021
- 35 F-THYRO1001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626
- 40 F-THYRO 1001809
- 45 F-THYRO1001828//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526
- F-THYRO1001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//AC003664
- 50 F-THYRO1001895
- 4.4e-13:248:68//AB012576
- 55 F-THYRO1001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058



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- 5 F-VESEN1000122//HS\_3075\_B1\_C09\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-  
16:130:90//AQ143749
- F-Y79AA1000013
- 10 F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete  
sequence.//2.9e-95:300:94//AC006027
- 15 F-Y79AA1000037//Human prot-oncogene (BML-1) mRNA, complete cds.//2.4e-19:230:  
66//L13689
- 20 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-  
38:629:64//U78521
- F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers  
DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:117:83//Z72005
- 25 F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893
- F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3  
Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2  
30 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-165:732:99//AL031864
- F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete  
35 sequence.//9.1e-20:339:65//AC005115
- F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33  
unordered pieces.//3.7e-72:397:93//AC004854
- 40 F-Y79AA1000230
- F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:  
45 90//AF053232
- F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SAcP-1)  
gene, complete cds.//0.0099:547:58//U78522
- 50 F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//4.0e-11:424:62//AF035207
- F-Y79AA1000313
- 55 F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20,  
genomic survey sequence.//5.9e-07:173:69//B55085

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F-Y79AA1000342//RPCI11-57J6.TK.1 RPCI11 Homo sapiens genomic clone R-57J6, genomic survey sequence.//5.2e-27:151:99//AQ115511

5 F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987

10 F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692

F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-21:129:85//AC005484

15 F-Y79AA1000368//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c.//0.00016:53:98//Z56610

20 F-Y79AA1000405//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747

25 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061

F-Y79AA1000420//H.sapiens CpG island DNA genomic Mse1 fragment, clone 82c3, forward read cpg82c3.ft1a.//2.0e-36:194:98//Z63378

30 F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736

35 F-Y79AA1000480//HS\_2175\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=O, genomic survey sequence.//2.5e-26:178:89//AQ307693

40 F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.67:111:72//AC004980

45 F-Y79AA1000539//HS\_2237\_B2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence.//1.2e-14:168:77//AQ153503

50 F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.94:127:67//AC005193

F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84//X14972

55 F-Y79AA1000574//M.musculus tex23 mRNA (5'region).//1.8e-23:291:75//X80424

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//8.6e-153:755:97//AF091080

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- 5 F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//5.2e-135:644:98//AF060503
- F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-148:902:86//X69942
- 10 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds.//4.8e-180:850:98//AB018080
- F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5.//0.00019:308:60//U23172
- 15 F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//1.7e-40:513:68//AJ003023
- 20 F-Y79AA1000774
- F-Y79AA1000782
- 25 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//3.5e-177:847:97//AF098799
- 30 F-Y79AA1000794//H.sapiens CpG island DNA genomic Mse1 fragment, clone 45a4, forward read cpg45a4.ft1a.//2.5e-13:104:92//Z61120
- F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//0.98:244:60//AF056085
- 35 F-Y79AA1000802
- F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//9.3e-76:528:85//U73642
- 40 F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence.//4.4e-14:99:95//B84538
- 45 F-Y79AA1000827//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//1.5e-08:249:69//AL022315
- 50 F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757
- F-Y79AA1000850
- 55 F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203
- F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete

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cds.//9.7e-150:865:89//AF071314

5 F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253

10 F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397

F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1.//4.3e-06:130:73//U88165

15 F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4e-44:428:77//U05823

F-Y79AA1001023

20 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3e-13:90:100//U63329

25 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds.//2.6e-28:772:60//D43682

F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence.//9.4e-36:292:82//AC004701

30 F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].//0.17:537:59//S64314

35 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds.//0.17:231:64//D88452

F-Y79AA1001078

40 F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//3.1e-63:529:77//D26173

45 F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.3e-23:228:76//AC005015

F-Y79AA1001167

50 F-Y79AA1001177//M.musculus mRNA for NfiX1-protein.//4.0e-10:398:64//Y07688

55 F-Y79AA1001185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//1.1e-113:666:90//Z93015

F-Y79AA1001211//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//5.5e-

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12:87:96//AQ187492

F-Y79AA1001216

5

F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//0.028:188:67//AL021841

10

F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds.//3.5e-24:731:60//M36263

15

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//1.2e-133:441:97//AJ005892

20

F-Y79AA1001281//HS\_2241\_B2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence.//5.0e-27:169:94//AQ217497

25

F-Y79AA1001299//Human Ini1 mRNA, complete cds.//6.7e-115:323:93//U04847

F-Y79AA1001312

F-Y79AA1001323

30

F-Y79AA1001384

35

F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//5.8e-42:245:74//U59322

40

F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence.//7.8e-18:636:58//Z48583

F-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-110:738:85//AC005924

45

F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497

50

F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95//AL034430

F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.7e-100:820:78//D14336

55

F-Y79AA1001541//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//5.1e-28:218:86//AQ150183

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- 5 F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence.//5.4e-21:167:86//AC004151
- F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:463:59//X59267
- 10 F-Y79AA1001581//FMR1 (CGG repeats) [human, Fragile X syndrome patient, Genomic, 429 nt].//0.00051:252:65//S74494
- F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds.//7.2e-33:375:76//M26434
- 15 F-Y79AA1001594
- F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861
- 20 F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583
- 25 F-Y79AA1001647//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860
- 30 F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.99:273:63//Z84468
- 35 F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//1.2e-97:682:81//M22743
- F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4].//5.6e-05:426:59//S37712
- 40 F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polypeptide (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136
- 45 F-Y79AA1001705//M.musculus fkh-5 gene.//0.18:153:64//X71943
- 50 F-Y79AA1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240
- F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017
- 55 F-Y79AA1001805//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse

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read cpg13d12.rt1c.//2.6e-13:88:100//Z64565

5 F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//3.7e-130:775:88//U74297

10 F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369

F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388

15 F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds.//6.9e-41:441:71//U41164

20 F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779

25 F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654

F-Y79AA1001923//H.sapiens CpG island DNA genomic Mse1 fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186

30 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184

35 F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340

40 F-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 526I14, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214

F-Y79AA1002089

45 F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548

50 F-Y79AA1002103//HS\_3052\_B1\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014

F-Y79AA1002115

55 F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693

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F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358

5 F-Y79AA1002204//HS\_2235\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260

10 F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397

15 F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719.

20 F-Y79AA1002210//Homo sapiens chromosome . 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615

F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043

25 F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738

30 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045

F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592

35 F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015

40 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555

45 F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886

F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534

50 F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877

55 F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101

F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208



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F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.0e-159:411:100//AC005920

5

F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//1.1e-118:609:84//AC004662

10

F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//4.4e-90:529:88//U49385

15

F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196

20

F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917

25

F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116

30

F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022

35

F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

### Homology Search Result Data 3.

35

The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.

Data include

40

the name of clone,

definition of the top hit data,

45

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

50

Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

55

Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:

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78//L16953

- 5 R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//Z88864
- 10 R-HEMBA1000042//RPCI11-77G23.TV RPCI11 Homo sapiens genomic clone R-77G23, genomic survey sequence.//1.3e-56:292:97//AQ268240
- 15 R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//J82696
- 20 R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948
- 25 R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-41:364:79//AC005520
- 30 R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//4.7e-30:229:84//AC003684
- 35 R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//AC003104
- 40 R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340
- 45 R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060
- 50 R-nnnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631
- 55 R-HEMBA1000158
- 60 R-nnnnnnnnnnnnn
- 65 R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904
- 70 R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146
- 75 R-HEMBA1000193
- 80 R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126
- 85 R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655

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- 5 R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548
- R-nnnnnnnnnnnn
- 10 R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181
- R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526
- 15 R-HEMBA1000244
- R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262
- 20 R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012
- 25 R-nnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037
- 30 R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270
- R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046
- 35 R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//AC004223
- 40 R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105
- 45 R-nnnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131
- R-nnnnnnnnnnnn//Rattus norvegicus Ca<sup>2+</sup>-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802
- 50 R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein.//3.8e-36:315:68//Y10496
- 55 R-nnnnnnnnnnnn//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC005505

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R-HEMBA1000338//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//2.0e-33:399:72//AL031667

5 R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//1.7e-39:272:87//AJ003147

10 R-HEMBA1000355//Human primary Alu transcript.//0.0045:67:85//U67829

R-HEMBA1000357//Homo sapiens (subclone 9\_h8 from PI H16) DNA sequence.//8.7e-93:426:88//L42086

15 R-HEMBA1000366//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-12:130:83//AC006012

20 R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//1.9e-69:355:97//AL031587

25 R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//3.7e-66:410:89//AC006116

30 R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:363:81//AC002993

35 R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//AC005053

R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//AC004582

40 R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575

45 R-HEMBA1000411

50 R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465

R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey sequence.//4.4e-12:98:92//AQ078233

55 R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//2.0e-93 :526:90//Z95400

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- R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-07:452:60//AC004826
- 5 R-HEMBA1000442//E.caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733
- R-HEMBA1000456//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//2.6e-05:174:70//AL010226
- 10 R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, complete cds; and unknown genes.//0.013:212:63//AF049236
- 15 R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//AC004839
- R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence.//0.086:334:61//Z83220
- 25 R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//AC005104
- 30 R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500
- R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278
- 35 R-HEMBA1000491
- R-HEMBA1000504//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//1.7e-08:440:60//AL009014
- 40 R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858
- 45 R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//1.1e-25:248:80//Z70280
- 50 R-HEMBA1000518//RPCI11-6022.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6022, genomic survey sequence.//0.0035:293:61//B49544
- 55 R-HEMBA1000519

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R-HEMBA1000520//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.30:255:63//AC006232

5 R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782

10 R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638

15 R-HEMBA1000540//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103

20 R-nnnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555

25 R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381

30 R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762

R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368

35 R-HEMBA1000568//RPCI11-49P8.TK.1 RPCI11 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293

40 R-nnnnnnnnnnnnn

R-HEMBA1000575//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335

45 R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573

50 R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:9411AJ007509

55 R-HEMBA1000592//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216

R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044

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- 5 R-HEMBA1000604//HS\_2220\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-  
51:306:92//AQ151991
- R-HEMBA1000608
- 10 R-HEMBA1000622//H.sapiens CpG island DNA genomic Mse1 fragment, clone 155e4,  
reverse read cpg155e4.rt1a.//4.5e-16:105:98//Z56962
- 15 R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome  
region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008
- 20 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:  
97//AB014590
- R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete  
sequence.//9.8e-61:311:90//AC005953
- 25 R-HEMBA1000657
- R-HEMBA1000662
- 30 R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1  
contains ESTs and STS.//1.0e-13:351:63//Z97196
- 35 R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//1.2e-50:298:79//AC005377
- 40 R-HEMBA1000686//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey  
sequence.//0.00048:210:62//AQ093513
- 45 R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//9.7e-54:317:88//AC005000
- R-HEMBA1000705//Glossonotus uhivittatus 12S mitochondrial ribosomal RNA, small  
subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850
- 50 R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:  
58//D50864
- 55 R-HEMBA1000722
- R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete  
sequence.//4.4e-26:284:77//AC005531

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- R-HEMBA1000727//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
contig 4-89, complete sequence.//9.1e-05:351:60//AL010266
- 5 R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21.  
Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism,  
complete sequence.//2.5e-16:123:93//AL021326
- 10 R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327O24, complete  
sequence.//2.8e-32:298:79//AC003108
- 15 R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11.  
Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2,  
ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:  
90//Z92545
- 20 R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete  
sequence.//2.7e-36:405:75//AC005031
- 25 R-HEMBA1000773//HS\_3050\_A2\_B08\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey  
sequence.//0.00053:268:60//AQ105619
- 30 R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete  
sequence.//4.7e-46:338:85//AC004690
- 35 R-HEMBA1000791//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-  
47:279:91//U14571
- R-HEMBA10008177//Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339
- 40 R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:  
61//Z15118
- 45 R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA,  
complete cds.//6.9e-43:228:98//AF048977
- 50 R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome  
20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-  
Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-  
Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable  
Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains  
a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:  
84//AL022394
- 55 R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence,



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complete sequence.//0.40:168:67//AC004260

5 R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

10 R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938

15 R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

20 R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

25 R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

30 R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP Homo sapiens genomic clone 2373I4, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

35 R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

40 R-HEMBA1000919

45 R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

50 R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//9.0e-113:586:95//AC005324

55 R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

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R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096

5 R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

10 R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

15 R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

20 R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

25 R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888

30 R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632

35 R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952

R-HEMBA1001007

40 R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365

R-HEMBA1001009//O.sativa osr40g2 gene.//0.99:203:62//Y08987

45 R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937

50 R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547

55 R-HEMBA1001020//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722

R-HEMBA1001022

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R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717

5 R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363

10 R-nnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686

15 R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217

R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751

20 R-HEMBA1001060//HS\_2056\_B1\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004

25 R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-I.//6.9e-38:513:70//X52046

30 R-HEMBA1001077//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318

R-HEMBA1001080

35 R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586

40 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607

R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105

45 R-HEMBA1001099

50 R-HEMBA1001109//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527

R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833

55 R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551

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R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511

R-HEMBA1001133

5

R-HEMBA1001137//Homo sapiens full-length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241

10

R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077

15

R-HEMBA1001172//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304

20

R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398

R-HEMBA1001197

25

R-HEMBA1001208//HS\_2233\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789

30

R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377

35

R-HEMBA1001235//RPCI11-50E6.TJ RPCI11 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666

40

R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905

45

R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//9.9e-21:537:63//AC004491

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R-HEMBA1001286

R-HEMBA1001289

55

R-HEMBA1001294//HS\_3219\_A2\_G01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882

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- R-HEMBA1001299//Homo sapiens, clone hRPK.12\_A\_1, complete sequence.//1.3e-38:381:76//AC006222
- 5
- R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258
- 10
- R-HEMBA1001303//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744
- R-HEMBA1001310
- 15
- R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504
- 20
- R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240
- R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete
- 25
- sequence.//2.2e-14:277:69//AL021368
- 30
- R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete
- 35
- sequence.//0.15:360:6//AL024509
- R-HEMBA1001330//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216
- 40
- R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete
- 45
- sequence.//7.1e-45:252:94//AC006238
- R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete
- sequence.//1.4e-113:569:97//AC006241
- 50
- R-HEMBA1001375//Homo sapiens full-length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542
- R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865
- 55
- R-HEMBA1001383

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R-HEMBA1001387

5 R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15  
unordered pieces.//8.9e-06:108:83//AC005073

10 R-HEMBA1001391//Yeast mitochondrial aapl gene for ATPase subunit 8.//7.3e-08:500:  
59//X00960

15 R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28,  
WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050

R-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
50024, WORKING DRAFT SEQUENCE.//5.5e-35 :464:68//AL034380

20 R-HEMBA1001407

25 R-HEMBA1001411//Yeast (S.cerevisiae) mitochondria Ser-tRNA-UCN gene and  
flanks.//0.00029:301:62//K01981

R-HEMBA1001413

30 R-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
41018, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732

35 R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//6.3e-37:302:81//AC006146

40 R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2.  
Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1  
of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:  
79//Z97054

45 R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related  
locus, complete sequence.//5.7e-59:457:82//AC004527

50 R-HEMBA1001442//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3.  
Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA  
repeat.//0.051:276:63//Z98950

55 R-HEMBA1001446//HS\_3207\_A1\_A08\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-  
06:119:73//AQ175385

R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete  
sequence.//0.0043:266:63//AC005065

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- 5 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete  
sequence.//7.1e-25:210:82//AC004855
- R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete  
sequence.//2.7e-08:316:62//AC005324
- 10 R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete  
sequence.//0.57:219:60//AC005208
- 15 R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//9.3e-50:252:80//AC004840
- R-HEMBA1001478
- 20 R-HEMBA1001497
- R-HEMBA1001510//Human HLA class III region containing cAMP response element binding  
protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds,  
25 complete sequence.//3.5e-41:282:86//U89337
- R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22.  
Contains EST and STS.//1.9e-79:529:86//Z98753
- 30 R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete  
sequence.//4.3e-18:335:71//AC004549
- 35 R-HEMBA1001522
- R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of  
the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands,  
40 .//5.6e-08:265:67//Z98258
- R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1.  
Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-  
45 16:235:72//Z97053
- R-HEMBA1001557
- 50 R-HEMBA1001566//Human Chromosome X clone bW XD187, complete sequence.//2.2e-44:  
416:78//AC004383
- R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040
- 55 R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete  
sequence.//1.1e-44:316:87//AC004453

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- 5 R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506
- R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276
- 10 R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6.//0.68:224:62//U41012
- R-HEMBA1001589
- 15 R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-69:337:99//AQ060483
- 20 R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177
- R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693
- 25 R-nnnnnnnnnnnn//HS\_2195\_A1\_E09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688
- 30 R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270
- 35 R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS.//6.0e-49:404:79//Z84484
- 40 R-nnnnnnnnnnnn
- R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368
- 45 R-HEMBA1001658//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808
- 50 R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740
- 55 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247
- R-HEMBA1001675



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- R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962
- 5 R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593
- 10 R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801
- 15 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598
- R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886
- 20 R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65/B32577
- 25 R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250
- 30 R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781
- 35 R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261
- R-HEMBA1001731//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799
- 40 R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959
- 45 R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067
- 50 R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084
- 55 R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153
- R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete

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sequence.//3.8e-39:331:80//AC006121

- 5 R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554
- 10 R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740
- 15 R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575
- 20 R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222
- 25 R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506
- 30 R-nnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977
- 35 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969
- 40 R-HEMBA1001809
- 45 R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025
- 50 R-HEMBA1001819//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612
- 55 R-HEMBA1001820//HS\_3022\_B1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence.//0.00054:335:59//AQ165107
- 60 R-nnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118
- 65 R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107
- 70 R-HEMBA1001835//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507
- 75 R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-

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07:170:68//U50871

R-HEMBA1001847

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R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517

10

R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

15

R-HEMBA1001866//HS\_2258\_B2\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138

20

R-nnnnnnnnnnn//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//5.9e-56:303:94//AC005065

25

R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.7e-43:281:88//AC006210

R-HEMBA1001896

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R-HEMBA1001910

R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.10:307:61//AC004775

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R-HEMBA1001913

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R-HEMBA1001915//HS\_2037\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence.//0.071:206:64//AQ233106

45

R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.97:449:59//AC004775

50

R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.0e-105:534:96//AF000145

R-HEMBA1001939//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508115, WORKING DRAFT SEQUENCE.//4.6e-13:120:82//AL021707

55

R-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-36:301:81//AC005629

R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence.//1.9e-10:

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208:68//AC003013

5 R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//1.2e-06:393:60//AE001433

10 R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R).//0.33:122:66//Z82646

R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds.//0.0086:427:59//U05329

15 R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//4.5e-07:176:70//AC004069

20 R-HEMBA1001964//HS\_2215\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence.//7.3e-25:215:74//AQ151931

25 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//1.7e-51:209:95//AL031178

30 R-HEMBA1001979//CIT-HSP-238712.TF.1 CIT-HSP Homo sapiens genomic clone 238712, genomic survey sequence.//4.9e-06:153:71//AQ240461

35 R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//3.1e-46:437:77//AL033521

40 R-HEMBA1001991//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-48:446:78//AL020997

45 R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta).//5.1e-90:448:97//AJ005801

50 R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.2e-42:317:84//Z97181

55 R-HEMBA1002018//HS\_3006\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic survey sequence.//1.0:63:74//AQ089717

R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453\_M\_1, complete sequence.//0.93:339:59//AC006203

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R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694

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R-HEMBA1002039

R-HEMBA1002049//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315

10

R-HEMBA1002084//CIT-HSP-2357L1.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey sequence.//0.0013:185:66//AQ063078

15

R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703

20

R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357

25

R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800

30

R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6e-64:550:80//U47924

R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-92:435:92//AC000378

35

R-HEMBA1002125

R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637

40

R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence.//2.0e-26:323:70//AC005728

45

R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide VB and (parts of) up to four novel genes, two with homology to Phorbolin genes and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG islands, complete sequence.//1.0:371:61//AL031846

50

R-HEMBA1002151

R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence.//2.4e-21:322:70//AC003971

55

R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2.

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Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1, ESTs and STS.//2.5e-38:216:84//Z97054

5

R-HEMBA1002161//CIT-HSP-2163F10.TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey sequence.//3.1e-58:284:80//B89969

10

R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence.//0.0079:286:57//Z80789

15

R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//5.9e-53:326:80//AC002980

R-HEMBA1002177

20

R-HEMBA1002185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING DRAFT SEQUENCE.//9.5e-37:356:76//AL033532

25

R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.4e-43:244:77//AC003684

30

R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.3e-37:323:78//AC005077

R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence.//1.4e-89:564:87//AC002498

35

R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.5e-31:313:71//AC000053

40

R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8.//0.0023:346:60//X57546

R-HEMBA1002215//M.musculus mRNA for testin.//4.7e-61:414:84//X78989

45

R-HEMBA1002226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.//4.6e-46:375:77//AL033529

50

R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.6e-46:238:98//AF089814

55

R-HEMBA1002237//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.3e-26:469:67//AC004242

R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//5.1e-23:162:82//AC005016

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R-HEMBA1002257

5 R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//4.6e-44:300:88//AF03 8127

10 R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence.//1.9e-19:176:85//AC000057

R-HEMBA1002321

15 R-HEMBA1002328//HS\_3061\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, genomic survey sequence.//1.0:151:65//AQ127617

20 R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, complete cds.//3.7e-07:328:63//U23811

25 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-128:642:96//AB018314

R-HEMBA1002348//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//3.7e-07:587:58//AL031256

30 R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment.//0.018:341:58//X02438

35 R-nnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:661:93//AF092563

40 R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11.//1.1e-70:559:79//AB020868

45 R-HEMBA1002389//HS\_3218\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602

50 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//AC005954

R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//AC004848

55 R-HEMBA1002430//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0023:604:56//X95276

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R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-23:183:80//AC006026

5 R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN. pseudogene similar to hnRNP A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819

10 R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378

15 R-HEMBA1002462//Sequence 43 from patent US 5708157.//2.0e-10:131:77//80068

R-nnnnnnnnnnnnn

20 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:80//AC004841

25 R-HEMBA1002486//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//U14573

R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey sequence.//1.0:122:68//AQ261762

30 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//2.8e-22:210:78//AC004963

35 R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//2.7e-17:435:58//AC003043

40 R-HEMBA1002508//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.7e-09:408:61//AC006213

R-nnnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972

45 R-HEMBA1002515

50 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923

R-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792

55 R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658



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- 5 R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378
- 10 R-HEMBA1002555//Homo sapiens full-length insert cDNA clone YR87G10.//8.3e-65:318:99//AF085957
- 15 R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409
- 20 R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.1e-44:192:80//AL008634
- 25 R-nnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587
- 30 R-HEMBA1002583
- 35 R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-42:248:88//Z95152
- 40 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//AC004510
- 45 R-HEMBA1002621
- 50 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351
- 55 R-HEMBA1002628//P.falciparum complete gene map of plastid-like DNA (IR-A).//8.8e-05:327:60//X95275
- R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence.//4.3e-06:205:66//AF046247
- R-HEMBA1002645//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.1e-39:281:84//U14567
- R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//1.1e-104:500:95//AC004839
- R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.2e-61:280:92//AL022323

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R-HEMBA1002661//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 225E12, WORKING DRAFT SEQUENCE.//3.2e-41:325:81//AL031772

5 R-HEMBA1002666//Homo sapiens full-length insert cDNA clone YY74A07.//0.00037:79:84//AF088008

10 R-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//2.3e-107:561:94//AL034421

R-nnnnnnnnnnnn//CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence.//5.4e-17:137:88//B99281

15 R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete sequence.//0.033:146:70//AC004503

20 R-HEMBA1002696

R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//6.2e-44:302:87//AC003982

25 R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds.//1.1e-31:332:76//AB004873

30 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.2e-35:287:81//AB014521

R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank.//0.018:233:66//M29109

35 R-HEMBA1002742//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE.//2.6e-13:419:62//AL033525

40 R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//0.019:202:65//AC003694

45 R-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.046:263:60//AL023883

R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs.//0.052:421:58//Z96810

50 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//1.2e-104:545:95//AB011126

55 R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC005140

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R-HEMBA1002777

5 R-HEMBA1002779//Human HepG2 3' region Mbol cDNA, clone hmd1e03m3.//9.4e-25:158:93//D17139

10 R-HEMBA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.6e-42:463:75//AL022344

15 R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence.//2.2e-05:417:59//AL034560

20 R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.//0.00055:444:59//L76261

25 R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//4.4e-115:559:97//AF071185

30 R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.3e-88:329:94//AC005043

35 R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//1.9e-22:262:67//AP000041

40 R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.3e-79:396:97//AC004707

45 R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.013:393:61//AC005506

50 R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//4.1e-73:489:85//AC005562

55 R-HEMBA1002876//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.21:549:55//AL034557

R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence.//0.30:431:56//B53836

R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds.//3.9e-106:541:95//AF037261

R-HEMBA1002921

R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium

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cancer, segment 7/10.//4.6e-19:139:78//AB020875

5 R-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
862K6, WORKING DRAFT SEQUENCE.//7.5e-45:282:89//AL031681

10 R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone  
2282P14, genomic survey sequence.//1.5e-102:514:97//AQ008584

R-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
745114, WORKING DRAFT SEQUENCE.//3.3e-87:444:97//AL033532

15 R-HEMBA1002939

20 R-HEMBA1002944//HS\_3107\_A1\_C05\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-  
21:250:73//AQ103952

25 R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene.//0.013:228:  
63//AJ008020

30 R-HEMBA1002954//HS\_3246\_A2\_G09\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-  
42:258:91//AQ218005

R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete  
sequence.//4.2e-38:300:83//AC005553

35 R-HEMBA1002970//Slime mold (D.discoideum) prestalk D11 gene, complete cds.//5.0e-05:  
541:57//M11012

40 R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:  
99//AB014579

45 R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete  
sequence.//9.1e-36:520:69//AC006128

R-nnnnnnnnnnnnn//Homo Sapiens Chromosome X clone bWXD691, complete  
sequence.//0.00040:504:59//AC004386

50 R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA,  
complete cds.//3.7e-66:556:79//U19614

55 R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22,  
WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406

R-HEMBA1003033//Homo sapiens full-length insert cDNA clone ZC34B10.//4.6e-78:414:

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94//AF086194

5 R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026

10 R-HEMBA1003035//HS\_2008\_A2\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839

15 R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694

R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983

20 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182

25 R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962

30 R-HEMBA1003067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302

R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136

35 R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975

40 R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054

45 R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673

50 R-HEMBA1003083//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798

55 R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3-unordered pieces.//1.2e-43:281:88//AC006039

R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT

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SEQUENCE.//0.00037:421:59//Z82213

5 R-HEMBA1003098//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4,  
BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered  
pieces.//1.4e-30:303:78//AC005598

10 R-HEMBA1003117

R-HEMBA1003129//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329

15 R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete  
sequence.//3.9e-99:484:98//AC004472

20 R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22,  
genomic survey sequence.//2.0e-10:93:92//B99861

25 R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer  
Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024

R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:  
96//AJ005670

30 R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contains  
ESTs.//6.4e-35:364:70//Z83822

35 R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:  
77//X60459

R-HEMBA1003197

40 R-HEMBA1003199//HS\_2166\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2166 Col=23 Row=I, genomic survey  
sequence.//0.00026:271:61//AQ164162

45 R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3  
unordered pieces.//5.4e-44:291:83//AC005480

50 R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete  
sequence.//3.1e-10:293:62//AC000118

R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1  
unordered pieces.//1.0:118:69//AC006148

55

R-HEMBA1003220//HS\_3092\_B1\_F09\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0:

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00014:59:91//AQ128202

- 5 R-HEMBA1003222//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y43F8, WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393
- 10 R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey sequence.//0.42:167:64//B83610
- R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey sequence.//3.6e-36:195:81//AQ037231
- 15 R-HEMBA1003250//HS\_2168\_A2\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356
- 20 R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709
- R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//1.0e-32:255:84//AC002549
- 25 R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308
- 30 R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-34:286:74//AC002395
- R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.8e-53:428:83//AC005840
- 35 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109
- 40 R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey sequence.//2.9e-20:337:65//AQ003073
- 45 R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:97//I25662
- R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence.//0.00019:334:60//AB017061
- 50 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//AB001872
- 55 R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.60:274:61//AL022153

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R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//AC005099

5 R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.2e-44:268:90//AC005081

10 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//AF026029

15 R-HEMBA1003348//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567

R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence.//0.00012:465:59//Z79600

20 R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//AC002558

25 R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.4e-34:375:74//AL022721

35 R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//1.6e-46:309:88//AC004651

40 R-HEMBA1003380//HS\_3184\_B2\_E06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=12 Row=J, genomic survey sequence.//1.0e-35:237:88//AQ189144

45 R-HEMBA1003384//HS\_2193\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic survey sequence.//0.00029:96:76//AQ032212

R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993

50 R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey sequence.//0.99:144:61//B91549

55 R-nnnnnnnnnnnnn

R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:98//AL031321



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- 5 R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//0.082:352:59//AC004879
- R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds.//9.9e-114:544:98//AF058696
- 10 R-HEMBA1003461
- R-HEMBA1003463
- 15 R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//9.1e-106:533:96//AC005041
- R-HEMBA1003528
- 20 R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//3.4e-08:333:64//AC002454
- 25 R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:333:68//X04701
- R-HEMBA1003545//Zebrafish mRNA for zfls1-2 (insulin gene enhancer binding protein homolog), complete cds.//0.030:144:68//D38453
- 30 R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0017:487:57//AC004153
- 35 R-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL031718
- R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC005913
- 40 R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.24:116:67//AF034416
- 45 R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.9e-05:422:63//AC006036
- R-HEMBA1003569//Homo sapiens full-length insert cDNA clone ZD82D06.//8.7e-108:545:95//AF086450
- 50 R-HEMBA1003571//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//4.6e-51:570:71//AC004914
- 55 R-HEMBA1003579//HS\_3237\_B2\_E05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic survey sequence.//8.5e-

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97:495:95//AQ209302

R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123

5

R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence.//2.9e-87:251:95//AC005774

10

R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//4.5e-52:384:83//AL008715

15

R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.6e-41:442:74//Z84480

20

R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.8e-23:177:88//AC005153

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R-HEMBA1003615

30

R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:494:57//AC005139

35

R-HEMBA100362111\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052122; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.3e-26:309:75//AC004599

40

R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//7.1e-56:545:75//AC002980

45

R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence.//2.8e-32:546:68//AF088219

50

R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//8.0e-25:457:68//AC002454

55

R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete sequence.//2.8e-40:280:86//AF031078

R-HEMBA1003645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693

R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//0.44:319:59//AL034559

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- 5 R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-36:242:80//AC004382
- R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.6e-117:588:96//AC005746
- 10 R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.8e-21:170:88//12222
- R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065
- 15 R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313
- R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872
- 20 R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466
- 25 R-HEMBA1003692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707
- 30 R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC000406
- R-HEMBA1003714
- 35 R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136
- 40 R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces.//2.4e-36:350:78//AC002353
- R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699
- 45 R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey sequence.//1.0:234:62//B86158
- 50 R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634
- 55 R-HEMBA1003742//HS\_3080\_B2\_H06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179

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- 5 R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG island.//4.5e-59:521:75//Z97876
- R-HEMBA1003760
- 10 R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343
- R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259
- 15 R-HEMBA1003784
- R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1 e-49:390:72//AC004455
- 20 R-HEMBA1003803
- 25 R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//9.4e-99:359:99//AC004596
- R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781
- 30 R-HEMBA1003807//Bovine dinucleotide microsatellite HUII77.//5.4e-18:194:78//M96348
- R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F2545L and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115
- 40 R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196624
- R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//4.8e-33:486:68//Z93929
- 50 R-HEMBA1003864//, complete sequence.//4.4e-100:531:94//AC005300
- 55 R-HEMBA1003866//HS\_3203\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298

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- 5 R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1,  
WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207
- R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28,  
WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036
- 10 R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:  
299:87//U32576
- 15 R-HEMBA1003893//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421
- 20 R-HEMBA1003902//HS\_3031\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-  
50:293:93//AQ165549
- 25 R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7,  
genomic survey sequence.//1.2e-32:220:92//AQ076795
- R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158),  
complete sequence.//3.1e-58:294:85//AC005368
- 30 R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:  
93//AF109718
- 35 R-HEMBA1003939
- R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:  
58//AC004904
- 40 R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial  
gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619
- 45 R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:  
57//AL034560
- 50 R-HEMBA1003958//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668
- R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase  
(ahybadh4) gene, complete cds.//0.11:428:60//AF000132
- 55 R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete  
sequence.//1.0:222:62//AC004414

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R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//80060

5 R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804

10 R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924

R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484

15 R-HEMBA1004000

R-HEMBA1004011

20 R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.7e-38:284:85//AC005670

25 R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575

30 R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081

35 R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054

R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.00071:263:68//AC006016

40 R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143

45 R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283

50 R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677

R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504

55 R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484

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R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952

5 R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76237

R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234

10 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

15 R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence.//6.0e-49:491:76//AC003665

20 R-HEMBA1004133//HS\_3229\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003

25 R-HEMBA1004138//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498

R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL008970

30 R-HEMBA1004146//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820

35 R-HEMBA1004150//CITBI-E1-2517I2.TR CITBI-E1 Homo sapiens genomic clone 2517I2, genomic survey sequence.//0.56:379:59//AQ277616

40 R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence.//4.6e-49:448:77//AC002429

R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-110:563:96//AF067855

45 R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z66569

50 R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//6.3e-30:293:77//AC004552

R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].//3.0e-64:517:80//S72304

55 R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.0e-97:303:98//AC005488

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- R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.6e-116:573:97//U50748
- 5 R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes.//5.4e-11:493:60//M37275
- 10 R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//6.1e-76:443:86//AF095927
- 15 R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence.//1.1e-42:330:83//AC005763
- R-HEMBA1004241
- 20 R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:288:85//AP000011
- R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.2e-09:516:61//AC004903
- 25 R-HEMBA1004264
- 30 R-HEMBA1004267//HS\_2255\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=O, genomic survey sequence.//8.6e-59:318:95//AQ068854
- 35 R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-113:576:96//AC005831
- 40 R-nnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence.//4.4e-110:553:96//AF091081
- R-HEMBA1004276
- 45 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//1.9e-106:538:97//AF022795
- 50 R-HEMBA1004289//RPCI11-74010.TJ RPCI11 Homo sapiens genomic clone R-74O10, genomic survey sequence.//2.3e-37:248:76//AQ266668
- R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:273:64//L13174
- 55 R-HEMBA1004306//HS\_3175\_B2\_F01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence.//1.6e-28:190:77//AQ169206



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R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence.//6.3e-36:267:82//AC003088

5 R-HEMBA1004321//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 10155, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611

10 R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//2.7e-42:136:91//AQ114933

15 R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence.//1.0:78:67//AQ017600

R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-119:580:98//AC004987

20 R-HEMBA1004334//Pimpinella brachycarpa Phybl mRNA, complete cds.//3.3e-14:238:69//AF082024

25 R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.8e-21:291:71//AC004638

R-HEMBA1004341

30 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds.//4.1e-74:444:90//D89667

35 R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.//7.0e-38:287:82//AC003002

R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//58611

40 R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446:63//AC005949

45 R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey sequence.//0.010:334:61//B55811

50 R-HEMBA1004389//Homo sapiens full-length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540

R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repeat.//1.0:50:84//X58124

55 R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:69//AC004057

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R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//AC005030

5 R-HEMBA1004408

R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200

10

R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-32:460:68//AJ011930

15 R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.9e-113:581:96//AC004846

20 R-HEMBA1004461//HS\_3244\_A2\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876

25 R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//AC006012

R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:513:59//AE001370

30

R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-08:245 :66//AC005951

35 R-HEMBA1004506//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487

40 R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266

R-HEMBA1004509

45 R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230

50 R-HEMBA1004538//HS\_3189\_B2\_C03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330

55 R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey sequence.//1.7e-16:116:93//B73329

R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457

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R-HEMBA1004573

5 R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:60//Z68279

10 R-HEMBA1004586

R-nnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551

15

R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071

20 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501.//1.4e-50:327:85//AB007970

R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//4.4e-13:527:63//AC004805

25

R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866

R-HEMBA1004632

30

R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-117:573:98//AC005534

35

R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076

R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//0.00013:501:58//AC005171

40

R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571:98//AL031432

45

R-HEMBA1004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE.//4.4e-12:110:88//Z93241

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R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//Z99291

55

R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.86:309:57//AB006702

R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic

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survey sequence.//0.29:331:61//B97342

- 5 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559
- 10 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-49:497:76//AC004638
- 15 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.6e-38:362:79//AC005562
- 20 R-HEMBA1004725
- R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:79//AC002085
- 25 R-HEMBA1004733
- R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island, ESTs, STS; and GSSs, complete sequence.//0.0030:362:61//AL022395
- 30 R-HEMBA1004736//Homo sapiens clone DJ0981O07, complete sequence.//1.9e-58:282:87//AC006017
- 35 R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:81//AC004953
- 40 R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950
- 45 R-HEMBA1004752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 495010, WORKING DRAFT SEQUENCE.//3.3e-39:281:85//AL031121
- 50 R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//L06498
- 55 R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island.//1.8e-08:516:59//AL021807
- 55 R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:72//AC004057

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R-HEMBA1004763

5 R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25.  
Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40  
ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC  
2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains  
ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310

10

R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete  
sequence.//8.7e-05:476:61//AE001371

15

R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human  
cosmid library) complete sequence.//5.0e-08:113:80//AC003047

R-HEMBA1004776

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R-HEMBA1004778//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-  
35:288:84//U14567

25

R-nnnnnnnnnnnn/HS\_3192\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-  
44:233:98//AQ155855

30

R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:  
87//AF048728

R-HEMBA1004806

35

R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//3.6e-20:333:69//AC005015

40

R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11.  
Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2,  
ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//6.3e-13:148:  
77//Z92545

45

R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:  
85//M74002

50

R-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68)  
.//7.6e-80:297:85//X53744

R-HEMBA1004850

55

R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter  
contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201

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R-HEMBA1004864

5 R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPC111-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297

10 R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826

15 R-HEMBA1004889//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943

R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//6.6e-11:144:7711AC005972

20 R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052

25 R-HEMBA1004918//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554

30 R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69//Y15994

R-HEMBA1004929

35 R-HEMBA1004930//Homo sapient chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848

R-HEMBA1004933//H.sapiens Humig mRNA.//0.13:233:62//X72755

40 R-HEMBA1004934//CIT-HSP-2021I16.TF CIT-HSP Homo sapiens genomic-clone 2021I16, genomic survey sequence.//0.66:268:62//B65345

45 R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849

50 R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341

R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408

55 R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249

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R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library *Oryza sativa* genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982

5 R-HEMBA1004973//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered  
10 pieces.//0.69:179:64//AC003656

R-HEMBA1004977//*Caenorhabditis elegans* cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495

15 R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete  
20 sequence.//0.20:427:60//AL024509

R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP *Homo sapiens* genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614

25 R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389

30 R-HEMBA1004995//*Homo sapiens* chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90:527:89//AC004224

35 R-HEMBA10050087//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix  
40 Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663

45 R-HEMBA1005009//*Homo sapiens* BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474

50 R-HEMBA1005019//*Homo sapiens* mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548

55 R-HEMBA1005029//*Homo sapiens* DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs,

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GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179

5 R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.4e-101:537:94//AC004596

10 R-HEMBA1005039//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650

R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819

15 R-HEMBA1005050//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library; complete sequence.//4.0e-43:371:80//AC002404

20 R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//2.3e-15:269:66//AC004675

R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-30:305:74//AC006030

25 R-HEMBA1005075

30 R-HEMBA1005079//Homo sapiens clone HS 19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156

R-HEMBA1005083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423

35 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//AF080561

40 R-HEMBA1005113//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340

45 R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//7.1e-55:306:82//AL022336

50 R-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//6.4e-45:309:87//AL022345

R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds.//3.2e-31:310:76//U81834

55 R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.//1.4e-33:361:79//AL021407



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R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence.//2.7e-22:440:66//AL031279

5 R-HEMBA1005185//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.0017:381:58//AL022594

10 R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.5e-05:457:57//X95276

R-HEMBA1005202//Human 18S ribosomal RNA.//4.7e-38:236:91//X03205

15 R-HEMBA1005219

20 R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//1.0:209:65//AC004854

R-HEMBA1005232//Homo-sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0040:439:58//AC004617

25 R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//4.2e-111:568:96//AC005154

30 R-HEMBA1005244//HS\_3092\_B2\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence.//4.9e-12:116:84//AQ127947

35 R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//3.2e-27:210:84//AC004548

40 R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.6e-105:437:97//AC005837

R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system.//0.011:339:59//D86630

45 R-HEMBA1005275//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//3.4e-17:269:71//AC004914

50 R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA, ESTs.//6.9e-20:193:73//Z75887

55 R-HEMBA1005296//HS\_3037\_B1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence.//0.26:184:64//AQ117120

R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7

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unordered pieces.//1.5e-58:445:78//AC006146

5 R-HEMBA1005311//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337

R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389

10 R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-40:409:71//AC006030

15 R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181

R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.9e-112:577:95//AC005803

20 R-HEMBA1005353//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722

25 R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412

30 R-HEMBA1005367//RPCI11-85E23.TV RPCI11 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915

R-HEMBA1005372//Homo sapiens full-length insert cDNA YH93B03.//2.6e-108:557:95//AF074997

35 R-HEMBA1005374//Homo sapiens full-length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142

40 R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tpx3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542

45 R-HEMBA1005394//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670

50 R-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379

55 R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958

R-HEMBA1005410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone

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732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722

5 R-HEMBA1005411//RPCI11-66N19.TK RPCI11 Homo sapiens genomic clone R-66N19,  
genomic survey sequence.//2.2e-38:222:79//AQ237442

10 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA,  
complete cds.//5.6e-117:453:99//AF041248

R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1  
contains ESTs and STS.//0.86:278:60//Z97196

15 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391

20 R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3.  
Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054

R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete  
sequence.//4.0e-27:469:66//AC004894

25 R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete  
sequence.//7.2e-40:410:76//AC005212

30 R-HEMBA1005472//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524

35 R-HEMBA1005475//HS\_2266\_B2\_C04\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:  
209:61//AQ069377

R-HEMBA1005497

40 R-HEMBA1005500//Homo sapiens PAC clone DJ1093O17 from 7q11.23-q21, complete  
sequence.//4.5e-116:580:97//AC004957

45 R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826

R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:  
59//AF003509

50 R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains  
CA repeats, STS.//0.44:195:63//Z96811

55 R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein  
(BICP4) gene, complete cds.//0.44:470:57//L14320

R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384

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- 5 R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-40:281:86//AC004913
- R-HEMBA1005526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73//Z97985
- 10 R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//3.8e-84:309:99//AB020860
- 15 R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//U84091
- 20 R-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431
- R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//AC004743
- 25 R-HEMBA1005558
- R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087
- 30 R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989
- 35 R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:631/AC005737
- 40 R-HEMBA1005577
- 45 R-HEMBA1005581//Homo sapiens mRNA for MEGFS, partial cds.//9.7e-27:561:64//AB011538
- R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171
- 50 R-HEMBA1005583//HS\_3014\_B1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499
- 55 R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced

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Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2, 6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046

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R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//2.2e-28:262:79//AC005746

10

R-HEMBA1005595//HS\_2224\_A2\_G03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence.//3.6e-48:263:95//AQ033446

15

R-HEMBA1005606//Human PAC clone DJ0093I03 from Xq23, complete sequence.//2.5e-08:355:63//AC003983

20

R-HEMBA1005609//HS\_2182\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130

25

R-HEMBA1005616//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176

30

R-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731

R-HEMBA1005627//Homo sapiens full-length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321

35

R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460

40

R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.4e-13:172:75//AL022069

45

R-HEMBA1005634//RPCI11-13O15.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13015, genomic survey sequence.//1.0e-28:153:82//B73293

50

R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786

55

R-HEMBA1005670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995

R-HEMBA1005679//Human esterase D mRNA, 3'end.//4.2e-49:322:88//M13450

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R-HEMBA1005680//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924

5 R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds.//5.4e-46:376:84//U66406

10

R-HEMBA1005705//RPCI11-13014.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13014, genomic survey sequence.//0.071:182:59//B76186

15 R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.0:189:66//Z92545

20

R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023

25 R-HEMBA1005737

R-nnnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255

30

R-HEMBA1005755//Human DNA-sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634

35 R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148

40 R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808

45

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805

50 R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559

R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:366:61//AC000124

55

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7

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and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.2e-107:551:96//AL031781

5

R-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aA4, genomic survey sequence.//2.6e-17:225:72//AL018730

10

R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence.//1.1e-27:314:75//AC000379

15

R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC006207

20

R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//2.0e-102:543:95//AC004945

R-HEMBA1005894

R-HEMBA1005909

25

R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence.//0.0012:315:60//AQ058081

30

R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z23072

35

R-HEMBA1005931//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304

40

R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261\_A\_13, complete sequence.//0.0052:179:71//AC005138

R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11:149:74//AC005045

45

R-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//5.4e-79:403:97//AQ147357

50

R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//6.9e-112:580:95//AF082516

55

R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285

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R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

5 R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035

10 R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405

15 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268

R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139

20 R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125

25 R-HEMBA1006042//HS\_2169\_A1\_B11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995

30 R-nnnnnnnnnnnn

R-HEMBA1006081

35 R-HEMBA1006090//HS\_2262\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=2 Row=A, genomic survey sequence.//2.1e-70:360:97//AQ216324

40 R-HEMBA1006091

45 R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains synapsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//1.6e-36:354:77//AL009172

R-HEMBA1006108

50 R-HEMBA1006121

R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327:64//Z95113

55 R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948



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R-nnnnnnnnnnnn//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80//AC005777

5 R-HEMBA100614211, complete sequence.//1.0e-13:160:78//AC005500

R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC004688

10

R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119:574:98//AF048693

15 R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:86//U28217

20 R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71//AC004491

R-HEMBA1006198//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567

25

R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557

30 R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567

35 R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//2.8e-41:438:71//U91323

R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384

40

R-HEMBA1006259//RPCI11-44N14.TJ RPCI11 Homo sapiens genomic clone R-44N14, genomic survey sequence.//1.5e-48:348:85//AQ203161

45 R-HEMBA1006268

50 R-HEMBA1006272//Human DNA sequence from clone 1198H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.//2.8e-73:273:87//AL023753

R-nnnnnnnnnnnn//H.sapiens PAP mRNA.//1.6e-54:585:71//X76770

55 R-HEMBA1006283//Sequence 7 from patent US 5776683.//9.7e-18:113:98//AR016240

R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete

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sequence.//0.97:447:59//AC004585

5 R-HEMBA1006291//Homo sapiens full-length insert cDNA clone ZB76B10.//2.9e-94:454:98//AF086161

R-HEMBA1006293//Sequence 8 from patent US 5721351.//8.1e-10:111:72//I89415

10 R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.6e-37:288:84//AC005412

15 R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.5e-29:132:81//AF076183

20 R-HEMBA1006328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 894K16, WORKING DRAFT SEQUENCE.//3.3e-50:340:75//AL034429

R-HEMBA1006334

25 R-HEMBA1006344//Rattus norvegicus nitzin mRNA, partial cds.//8.7e-22:259:72//AF087945

R-HEMBA1006347//Human prostatic gene, complete cds.//1.8e-78:170:100//U33446

30 R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, complete cds.//0.00051:120:73//M57682

35 R-HEMBA1006359//CITBI-E1-2516C16.TR CITBI-E1 Homo sapiens genomic clone 2516C16, genomic survey sequence.//4.7e-74:576:82//AQ277951

R-HEMBA1006364//G.gallus gene for transforming growth factor-beta2, exons 5-7.//2.5e-21:118:85//X59080

40 R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85//AC005239

45 R-HEMBA1006380//Human BAC clone RG007J15 from 7q31, complete sequence.//6.1e-47:300:83//AC003989

50 R-HEMBA1006381//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//1.5e-47:336:86//AC005914

R-HEMBA1006398//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.5e-67:501:83//AC005609

55 R-HEMBA1006416//Homo sapiens chromosome 17, clone 347\_H\_5, complete sequence.//4.4e-37:319:76//AC002119

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R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete sequence.//2.9e-50:502:75//AC004253

5 R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//4.1e-116:572:97//AF107885

10 R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//9.4e-117:578:97//AL031781

15 R-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//2.2e-08:353:63//Z93017

20 R-HEMBA1006438//HS\_2008\_A1\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey sequence.//1.2e-29:194:91//AQ245162

25 R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:330:60//AC005075

30 R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.032:256:61//AE001398

35 R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//5.6e-35:229:77//AC002364

R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence.//11.1e-14:354:63//AC002052

40 R-HEMBA1006471

45 R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3].//1.1e-14:442:60//S67502

R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//3.7e-37:290:82//U95742

50 R-HEMBA1006485//H.sapiens mRNA for aminopeptidase.//7.6e-91:517:91//Y07701

55 R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-33:289:81//AC005089

R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-

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11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//6.0e-07:485:60//AL020989

5 R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//4.3e-112:572:95//AC005828

10 R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.3e-10:186:67//AC002994

15 R-HEMBA1006497//RPCI11-16L10.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16L10, genomic survey sequence.//1.5e-10:75:100//B88015

20 R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.3e-36:516:70//Z93929

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//1.2e-115:570:96//AB014566

25 R-HEMBA1006521//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//2.2e-20:266:71//Z98304

30 R-HEMBA1006530//RPCI11-52M1.TJ RPCI11 Homo sapiens genomic clone R-52M1, genomic survey sequence.//0.00015:227:64//AQ052526

35 R-HEMBA1006535//HS\_2234\_B1\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence.//7.5e-33:191:95//AQ129525

40 R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence.//0.026:497:58//AC005007

R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence.//5.2e-41:289:86//AC004603

45 R-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//3.4e-64:551:78//U06944

50 R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//5.7e-09:266:66//AC002554

55 R-HEMBA1006566//HS\_2171\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence.//0.012:306:61//AQ125421

R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//3.8e-70:529:82//U39357

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- 5 R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence.//1.0:141:65//AC006032
- 10 R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875
- 15 R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709
- R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031
- R-HEMBA1006612
- 20 R-nnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737
- 25 R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284
- 30 R-HEMBA1006631//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848
- 35 R-HEMBA1006635//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572
- 40 R-HEMBA1006639
- R-HEMBA1006643
- 45 R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282
- 50 R-HEMBA1006652//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089
- R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390
- 55 R-HEMBA1006665//HS\_3213\_B2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625

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- 5 R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTELOO023.seq.//2.6e-32:212:83//Z96776
- R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551
- 10 R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608
- 15 R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096
- R-HEMBA1006696
- 20 R-HEMBA1006708
- R-HEMBA1006709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674
- 25 R-HEMBA1006717
- R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//9.9e-18:365:66//AC005828
- 30 R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.3e-37:380:75//AC003108
- 35 R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951
- 40 R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752
- 45 R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551
- R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.3e-46:305:87//AC005701
- 50 R-HEMBA10067801//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-39:305:82//AL022323
- 55 R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61//AL031317
- R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete

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sequence.//4.1e-43:355:801/AC006120

5 R-HEMBA1006796//HS\_3038\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:  
158:63//AQ102483

10 R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33  
unordered pieces.//8.4e-47:481:75//AC004854

15 R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete  
sequence.//3.0e-08:84:90//AC004797

R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome  
Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:496:76//Z93023

20 R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete  
sequence.//0.70:206:65//AC005668

25 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer  
Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217

30 R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence.//0.61:115:  
70//AF056074

R-nnnnnnnnnnnn//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-  
102:618:87//AB017026

35 R-HEMBA1006885 4.2e-14:379:63//AG006839

R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20,  
genomic survey sequence.//2.6e-07:230:66//B56395

40 R-HEMBA1006921//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete  
sequence.//2.1e-68:267:86//AC005154

45 R-HEMBA1006926

50 R-HEMBA1006929//HS\_3244\_A2\_C01\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-  
21:191:83//AQ207500

R-HEMBA1006936

55 R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial  
sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene,  
partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853

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- 5 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841
- R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518
- 10 R-HEMBA1006973//HS\_2009\_A2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302
- 15 R-HEMBA1006976//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701
- R-HEMBA1006993//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.9e-47:394:79//U18271
- 20 R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406
- 25 R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558
- 30 R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.6e-41:437:71//AC005277
- R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088
- 35 R-HEMBA1007045
- R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006
- 40 R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056
- 45 R-HEMBA1007062
- R-HEMBA1007066
- 50 R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//2.0e-66:476:85//AC006141
- 55 R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence.//1.0e-38:179:82//AC005325



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R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.2e-49:551:73//AC006015

5 R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1.0:261:61//AC000385

10 R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//0.043:295:62//AC004803

15 R-HEMBA1007113//Homo sapiens (subclone 6\_a8 from P1 H16) DNA sequence.//1.4e-52:307:87//L43392

R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547

20 R-HEMBA1007147//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65f1, reverse read cpg65f1.rt1a.//0.16:187:64//Z62246

25 R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//7.6e-108:543:96//AC005239

30 R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.14:323:58//AC004875

R-nnnnnnnnnnnn//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-103:529:94//AF062085

35 R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//5.4e-106:537:96//AC005911

40 R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.1e-39:262:80//AC003035

45 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.3e-61:332:95//D86987

R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//1.9e-50:436:81//Z93023

50 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.3e-96:471:97//AB018340

55 R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//0.011:349:62//AC004777

R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, complete

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sequence.//2.8e-10:224:70//AC004856

5 R-HEMBA1007267//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.4e-53:362:86//AC005924

R-HEMBA1007273

10 R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4.//0.042:454:57//AJ235273

15 R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.99:288:60//AJ235272

20 R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//7.4e-107:554:95//AL031003

R-HEMBA1007300//Caenorhabditis elegans cosmid C48C5.//0.22:474:59//U39994

25 R-HEMBA1007301

R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT.//4.9e-08:524:58//Y14425

30 R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//3.4e-16:244:71//AP000043

35 R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, complete sequence.//3.9e-83:383:85//AC005251

40 R-HEMBA1007327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 7706, WORKING DRAFT SEQUENCE.//1.6e-38:533:71//Z96804

R-HEMBA1007341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268D13, WORKING DRAFT SEQUENCE.//3.6e-21:394:66//AL023513

45 R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete sequence.//1.7e-15:190:73//AC003080

50 R-HEMBA1007347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone N38G6, WORKING DRAFT SEQUENCE.//2.2e-47:455:77//Z96802

55 R-HEMBA1000005//Homo sapiens 3p21.1-9 PAC RPCI4-793P23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-62:539:79//AC006208

R-HEMBA1000008//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence.//1.2e-36:285:83//AC003665

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- 5 R-HEM BB1000018//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-51:416:79//AC004820
- 10 R-HEM BB1000024//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//3.9e-18:211:79//Z95113
- 15 R-HEM BB1000025//HS\_3064\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=14 Row=D, genomic survey sequence.//5.9e-40:254:90//AQ132765
- 20 R-HEM BB1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete sequence.//1.5e-32:452:70//Z85986
- 25 R-HEM BB1000036//CIT-HSP-2024L15.TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey sequence.//9.3e-63:541:77//B66264
- 30 R-HEM BB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//7.6e-91:467:97//AF084928
- 35 R-HEM BB1000039//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//2.4e-44:456:68//AC005291
- 40 R-HEM BB1000044//Human BAC clone RG016J04 from 7q21, complete sequence.//1.4e-54:307:80//AC002064
- 45 R-HEM BB1000048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//3.8e-09:330:63//AC002300
- 50 R-HEM BB1000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056
- 55 R-HEM BB1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521
- 60 R-HEM BB1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806
- 65 R-HEM BB1000059//Homo sapiens clone DJ0850I01, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009
- 70 R-HEM BB1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

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- 5 R-HEMBB1000089//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520
- 10 R-HEMBB1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715
- 15 R-HEMBB1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115
- 20 R-HEMBB1000113//HS\_3013\_A1\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730
- 25 R-HEMBB1000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521
- 30 R-HEMBB1000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407
- 35 R-HEMBB1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945
- 40 R-HEMBB1000144//Homo sapiens chromosome 17, clone hCIT.507\_E\_2, complete sequence.//0.00083:206:66//AC004134
- 45 R-HEMBB1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085
- 50 R-HEMBB1000175
- 55 R-HEMBB1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368
- R-HEMBB1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

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R-HEM BB1000217

5 R-HEM BB1000218//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

10 R-HEM BB1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

15 R-HEM BB1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEM BB1000244//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

20 R-HEM BB1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777 R-HEM BB1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

30 R-HEM BB1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

35 R-HEM BB1000266//RPCI11-76C20.TV RPCI11 Homo sapiens genomic clone R-76C20, genomic survey sequence.//1.0:232:59//AQ265533

40 R-HEM BB1000272//HS\_3032\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ 096702

R-HEM BB1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.6e-45:277:72//AC000053

45 R-HEM BB1000284//Homo sapiens full-length insert cDNA clone YY88A05.//6.9e-112:572:96//AF088018

50 R-HEM BB1000307//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//5.7e-96:523:93//AC005244

55 R-HEM BB1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693

R-HEM BB1000317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145

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- 5 R-HEM BB1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710
- R-HEM BB1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179
- 10 R-HEM BB1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147
- 15 R-HEM BB1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329O10, genomic survey sequence.//1.2e-31:192:92//AQ035976
- R-HEM BB1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//1.9e-39:477:71//AC004605
- 20 R-HEM BB1000339//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031681
- 25 R-HEM BB1000341//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350
- 30 R-HEM BB1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence.//3.6e-41:457:72//AC004644
- 35 R-HEM BB1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751
- 40 R-HEM BB1000369//Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence.//9.0e-25:179:79//AC004067
- R-HEM BB10003741//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199
- 45 R-HEM BB1000376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675
- 50 R-HEM BB1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080
- 55 R-HEM BB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838
- R-HEM BB1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052

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- 5 R-HEM BB1000404//HS\_2246\_A2\_D01\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:  
196:63//AQ084251
- 10 R-HEM BB1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC  
Region, complete sequence.//1.2e-29:358:72//AC000053
- 15 R-HEM BB1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete  
sequence.//2.8e-51:299:89//AC004069
- 20 R-HEM BB1000438//HS\_2239\_B2\_E08\_MF CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-  
10:76:100//AQ067700
- 25 R-HEM BB1000441//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207
- R-HEM BB1000449//Homo sapiens clone DJ0898O18, WORKING DRAFT SEQUENCE, 8  
unordered pieces.//4.8e-11:228:68//AC004920
- 30 R-HEM BB1000455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14:388:  
65//AC005007
- 35 R-HEM BB1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete  
sequence.//4.9e-34:320:79//AC003104
- 40 R-HEM BB1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-  
qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5  
(sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter),  
complete sequence.//3.4e-36:285:82//Z83849
- 45 R-HEM BB1000487
- R-HEM BB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423
- 50 R-HEM BB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome  
Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023
- 55 R-HEM BB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-  
21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the  
60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for  
Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone  
Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs  
and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721

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- R-HEM BB1000510//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397
- 5 R-HEM BB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477
- 10 R-HEM BB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079
- 15 R-HEM BB1000530//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//4.2e-74:428:92//AC006236
- 20 R-HEM BB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.6e-13:112:80//U91321
- R-HEM BB1000554//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824
- 25 R-HEM BB1000556//Homo sapiens envoplakin (EVPL) mRNA, complete cds.//0.031:275:60//U53786
- 30 R-HEM BB1000564//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//3.1e-17:227:76//AC005914
- 35 R-HEM BB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed spacer.//0.078:161:63//D84405
- R-HEM BB1000575//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence.//7.2e-52:260:80//AC003695
- 40 R-HEM BB1000586//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280
- 45 R-HEM BB1000589//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//1.3e-14:409:65//AC005208
- 50 R-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184
- R-HEM BB1000592//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-08:254:64//AC005831
- 55 R-HEM BB1000598//Homo sapiens chromosome 11 pac pDJ159ol, complete sequence.//3.3e-38:407:76//AC000381



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R-HEM BB1000623//CIT-HSP-2374P17.TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence.//1.3e-41:212:100//AQ109717

5 R-HEM BB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724

10 R-HEM BB1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//180058

R-HEM BB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176

15 R-HEM BB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085

20 R-HEM BB1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112

25 R-HEM BB1000643//HS\_2242\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993

30 R-HEM BB1000649//Homo sapiens RBP56/hTAFII68 gene, exon 7.//8.3e-63:306:100//AB010061

35 R-HEM BB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat.//3.3e-14:450:64//AL009031

40 R-HEM BB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence.//0.98:251:63//AB005247

45 R-HEM BB1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chromosome X.//6.8e-58:296:85//Z83313

50 R-HEM BB1000673//CITBI-E1-2506F20.TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731

R-HEM BB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584

55 R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds.//2.0e-50:287:93//AF040723

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R-HEM BB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943

5 R-HEM BB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380

10 R-HEM BB1000709//RPCI11-79A8.TV RPCI11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374

15 R-HEM BB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence.//0.00018:386:60//AB017066

R-HEM BB1000726//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990

20 R-HEM BB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875

25 R-HEM BB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069

30 R-HEM BB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoter region and 5' coding region.//1.0:115:63//K02071

R-HEM BB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205

35 R-HEM BB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046

40 R-HEM BB1000789//RPCI11-2I14.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2I14, genomic survey sequence.//3.0e-09:299:64//B63628

45 R-HEM BB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740

50 R-HEM BB1000794//HS\_3253\_A1\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291

R-HEM BB1000807

55 R-HEM BB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542

R-HEM BB1000821

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- 5 R-HEM BB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944
- R-HEM BB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043
- 10 R-HEM BB1000827//Homo sapiens clone DJ0981O07, complete sequence.//6.8e-43:319:84//AC006017
- 15 R-HEM BB1000831//HS\_3247\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850
- 20 R-HEM BB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete
- 25 sequence.//4.2e-17:167:80//AL021368
- R-HEM BB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283
- 30 R-HEM BB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086
- 35 R-HEM BB1000852//HS\_3075\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816
- 40 R-HEM BB1000870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523
- 45 R-HEM BB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474
- 50 R-HEM BB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//AC005621
- R-HEM BB1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061
- 55 R-HEM BB1000888//CIT-HSP-2282A13.TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ000826

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- 5 R-HEMBB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995
- R-HEMBB1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492
- 10 R-HEMBB1000908//RPCI11-13P12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13P12, genomic survey sequence.//0.98:183:61//B76199
- 15 R-HEMBB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024
- R-HEMBB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037
- 20 R-HEMBB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 complete sequence.//6.3e-09:536:59//U95739
- 25 R-HEMBB1000917//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015
- R-HEMBB1000927
- 30 R-HEMBB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence.//0.090:115:69//B99228
- 35 R-HEMBB1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//5.7e-89:544:90//AC003098
- 40 R-HEMBB1000973//Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence.//0.038:377:58//AC005560
- 45 R-HEMBB1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence.//1.0e-05:342:62//AC006234
- 50 R-HEMBB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443
- 55 R-HEMBB1000985//HS\_3184\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008
- R-HEMBB1000991
- R-HEMBB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2

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gene exons 1,2, and 3, complete sequence.//1.4e-42:343:81//AC002368

R-HEM BB1001004

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R-HEM BB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056

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R-HEM BB1001011//HS\_3017\_B1\_G03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944

15

R-HEM BB1001014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662

20

R-HEM BB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549

25

R-HEM BB1001024//Homo sapiens (subclone 2\_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475

R-HEM BB1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence.//2.0e-50:416:82//AC005527

30

R-HEM BB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699

35

R-HEM BB1001051//H.sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586

R-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014

40

R-HEM BB1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187

45

R-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//U49973

50

R-HEM BB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING DRAFT SEQUENCE.//4.0e-114:556:98//AL034375

R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:512:97//AF034803

55

R-HEM BB1001096//Human DNA sequence from PAC 246O8, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735

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- 5 R-HEM BB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577
- 10 R-HEM BB1001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462023, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431
- 15 R-HEM BB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2),5'UTR. ESTs, STS.//1.1e-38:306:84//Z99570
- 20 R-HEM BB1001117//RPCI11-35I8.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35I8, genomic survey sequence.//1.5e-08:67:100//AQ047113
- R-HEM BB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071
- 25 R-HEM BB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495
- 30 R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//M25077
- 35 R-HEM BB1001137//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222
- R-HEM BB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564
- 40 R-HEM BB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
- 45 R-HEM BB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-10L7, genomic survey sequence.//2.3e-34:213:82//B71766
- 50 R-HEM BB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070
- 55 R-nnnnnnnnnnnn//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055
- R-HEM BB1001177
- R-HEM BB1001182//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226

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- R-HEM BB1001199
- 5 R-HEM BB1001208
- R-HEM BB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098
- 10 R-HEM BB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//6.2e-08:412:61//AC005199
- 15 R-HEM BB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//1.0e-46:498:74//B75158
- 20 R-HEM BB1001221//RPCI11-62024.TJ RPCI11 Homo sapiens genomic clone R-62024, genomic survey sequence.//3.2e-09:215:68//AQ200950
- R-HEM BB1001234
- 25 R-HEM BB1001242
- R-HEM BB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.4e-33:361:72//AC005377
- 30 R-HEM BB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//3.8e-105:517:98//AF042089
- 35 R-HEM BB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461
- 40 R-HEM BB1001267//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2, 6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046
- 45 R-HEM BB1001271//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//3.9e-47:494:75//AC005544
- 50 R-HEM BB1001282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428
- 55 R-HEM BB1001288
- R-HEM BB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180),

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complete sequence.//2.0e-31:301:78//AC005601

5 R-HEMBB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//0.053:283:60//AC003083

R-HEMBB1001302

10 R-HEMBB1001304//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//6.3e-15:396:64//AL033397

15 R-HEMBB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence.//3.4e-42:293:86//AG013777

R-HEMBB1001315//Human NFE genomic fragment.//7.5e-30:243:78//M98511

20 R-HEMBB1001317//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//2.3e-39:301:82//AC004585

25 R-HEMBB1001326//HS\_3054\_A1\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117:63//AQ106096

30 R-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//0.037:103:77//D63850

35 R-HEMBB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//9.1e-19:229:77//AC003037

R-HEMBB1001337

40 R-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//2.9e-45:551:72//U85056

45 R-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.7e-59:292:99//AF097441

R-HEMBB1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//9.1e-41:326:82//AC004859

50 R-HEMBB1001356//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//1.8e-11:213:67//Z82207

55 R-HEMBB1001364//HS\_3050\_A2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158:91//AQ133940



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R-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence.//4.1e-37:419:73//AC005876

5 R-HEM BB1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:75//J91326

10 R-HEM BB1001369//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 477J10, WORKING DRAFT SEQUENCE.//1.8e-28:224:83//AL021686

15 R-HEM BB1001380//HS\_2267\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2267 Col=21 Row=L, genomic survey sequence.//4.0e-14:100:95//AQ084896

20 R-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.6e-55:312:81//AF071314

R-HEM BB1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBNL H105), complete sequence.//1.0:166:63//AC003953

25 R-HEM BB1001394//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//1.4e-55:494:76//AC005549

30 R-HEM BB1001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.011:208:63//AC006204

35 R-HEM BB1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325:69//AC002370

R-HEM BB1001426//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-46:328:84//AC002350

40 R-HEM BB1001429//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550:95//AC006160

45 R-HEM BB1001436

50 R-HEM BB1001443//HS\_2228\_A1\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173:62//AQ066934

55 R-HEM BB1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.7e-23:339:69//AC005522

R-HEM BB1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.//1.1e-39:299:84//AC005355

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- 5 R-HEM BB1001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//6.0e-05:486:59//AE001430
- R-HEM BB1001463//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//1.2e-50:317:89//AC005154
- 10 R-HEM BB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941
- 15 R-HEM BB1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762
- 20 R-HEM BB1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801
- 25 R-HEM BB1001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332:75//AF046642
- R-HEM BB1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:483:76//AC005000
- 30 R-HEM BB1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159:71//AC002070
- 35 R-HEM BB1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.//4.0e-30:286:79//Z74581
- 40 R-HEM BB1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342:80//U73169
- R-HEM BB1001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361:77//AC000394
- 45 R-HEM BB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.//0.34:212:61//AC003049
- 50 R-HEM BB1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//8.0e-40:267:88//AC002301
- 55 R-HEM BB1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286:76//AC005225
- R-HEM BB1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12

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unordered pieces.//2.5e-15:194:75//AC004840

5 R-HEM BB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL031677

10 R-HEM BB1001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-30:371:74//AC005236

R-HEM BB1001588//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106

15 R-HEM BB1001603//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-59, complete sequence.//0.034:302:59//AL010235

20 R-HEM BB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and OpG island.//7.1e-31:503:68//Z93023

25 R-HEM BB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368

30 R-HEM BB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island genomic fragments.//1.3e-27:228:82//Z86062

R-HEM BB1001635//Homo Sapiens Chromosome X clone bW XD90, complete sequence.//1.5e-23:407:69//AC004075

35 R-HEM BB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368

40 R-HEM BB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506

45 R-HEM BB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344

50 R-HEM BB1001665//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572

R-HEM BB1001668

55 R-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546

R-HEM BB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//I86429

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- 5 R-HEMBB1001685//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//2.6e-43:31:83//AC005411
- R-HEMBB1001695
- 10 R-HEMBB1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259:58//AQ028704
- R-HEMBB1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296:80//AC004851
- 15 R-HEMBB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020
- 20 R-HEMBB1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992
- R-HEMBB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613
- 25 R-HEMBB1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221
- 30 R-HEMBB1001747//Homo sapiens cosmid Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671
- 35 R-HEMBB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.4e-60:242:92//AC005829
- R-HEMBB1001753//RPC111-59J22.TK RPC111 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046
- 40 R-HEMBB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130
- 45 R-HEMBB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050
- 50 R-HEMBB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157
- 55

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R-HEM BB1001785//*Torulopsis glabrata* mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:189:65//X02170

5 R-HEM BB1001797//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140

10 R-HEM BB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391

R-HEM BB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882

15 R-HEM BB1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996

20 R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209

25 R-HEM BB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328

R-HEM BB1001839

30 R-HEM BB1001850//*Arabidopsis thaliana* genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241

35 R-HEM BB1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436

R-HEM BB1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327

40 R-HEM BB1001868//*Arabidopsis thaliana* genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754

45 R-HEM BB1001869//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//7.0e-37:285:85//AC002553

50 R-HEM BB1001872//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//AL009027

R-HEM BB1001874

55 R-HEM BB1001875//*Lactococcus lactis* DPC3147 plasmid pMRC01, complete plasmid sequence.//0.037:406:60//AE001272

R-HEM BB1001880//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete

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sequence.//1.3e-49:461:77//AC005922

5 R-HEMBB1001899//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from  
clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z98858

10 R-HEMBB1001905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL022345

R-HEMBB1001906

15 R-HEMBB1001908//Genomic sequence from Human 17, complete sequence.//2.9e-36:274:  
76//AC001231

20 R-HEMBB1001910//Homo sapiens chromosome 17, clone HCIT39G8, complete  
sequence.//3.5e-41:408:76//AC003070

R-HEMBB1001911//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT  
SEQUENCE.//6.1e-64:310:89//AJ011929

25 R-HEMBB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds.//2.0e-20:220:  
78//D38417

30 R-HEMBB1001921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
1141E15, WORKING DRAFT SEQUENCE.//1.9e-47:410:80//AL034422

35 R-HEMBB1001922//Homo sapiens chromosome 17, clone HCIT421K24, complete  
sequence.//6.2e-32:378:74//AC004099

R-HEMBB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22,  
WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.2e-41:304:84//AC000406

40 R-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of  
hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//8.3e-12:202:  
69//AB020867

45 R-HEMBB1001944//P.falciparum gene for beta subunit RNA polymerase.//0.00090:264:  
62//X75544

50 R-HEMBB1001945//Swietenia humilis DNA for simple tandem repeat (242bp).//0.056:224:  
62//AJ000408

55 R-HEMBB1001947//RPCI11-60L13.TJ RPCI11 Homo sapiens genomic clone R-60L13,  
genomic survey sequence.//7.4e-23:146:94//AQ202335

R-HEMBB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains  
synapsin IIIa exon 1, EST and GSS, complete sequence.//0.57:115:68//Z83846

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- 5 R-HEM BB1001952//Homo Sapiens Chromosome X clone bW XD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-36:283:84//AC004676
- R-HEM BB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.9e-60:334:82//AC005037
- 10 R-HEM BB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.9e-56:518:77//AC005077
- 15 R-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//3.2e-19:157:86//AC005736
- R-HEM BB1001967//Homo sapiens DNA for amyloid precursor protein, complete cds.//5.7e-68:314:89//D87675
- 20 R-HEM BB1001973//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE.//1.4e-37:484:70//AJ009617
- 25 R-HEM BB1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL034417
- 30 R-HEM BB1001988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//6.9e-29:203:88//AL034420
- R-HEM BB1001990//Homo sapiens full-length insert cDNA clone ZC33G03.//7.8e-95:456:99//AF086192
- 35 R-HEM BB1001996
- R-HEM BB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces.//6.4e-26:162:83//AC005055
- 40 R-HEM BB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs.//8.2e-83:362:93//Z84816
- 45 R-HEM BB1002005//Homo sapiens chromosome 3p clone RPCI5-1034C16, WORKING DRAFT SEQUENCE, 45 unordered pieces.//8.5e-36:291:83//AC005903
- 50 R-HEM BB1002009//Homo sapiens clone DJ0828F13, complete sequence.//5.6e-08:307:65//AC004904
- 55 R-HEM BB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.9e-05:375:62//B36336

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R-HEM BB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 2313E13, genomic survey sequence.//0.34:241:62//AQ028389

- 5 R-HEM BB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.//7.4e-35:297:82//AC005612
- 10 R-HEM BB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.8e-96:582:90//AC005740
- 15 R-HEM BB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.7e-63:575:77//AC005778
- R-HEM BB1002049//Human Chromosome X clone bW XD187, complete sequence.1//1.9e-21:384:64//AC004383
- 20 R-HEM BB1002050//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//2.5e-37:368:76//AC005553
- 25 R-HEM BB1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//0.30:167:65//AC004782
- 30 R-HEM BB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.3e-73:449:84//AC004799
- R-HEM BB1002092//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//3.8e-45:307:87//AC005828
- 35 R-HEM BB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.1e-47:457:76//AC005943
- 40 R-HEM BB1002115//HS\_2223\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, genomic survey sequence.//3.0e-58:295:98//AQ152279
- 45 R-HEM BB1002139//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//6.6e-49:283:93//U14573
- 50 R-HEM BB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-45:451:76//AC006006
- R-HEM BB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10q25, complete sequence.//1.3e-57:359:81//AC005881
- 55 R-HEM BB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence.//4.5e-43:420:77//AC000385



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R-HEM BB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//8.2e-33:340:64//AC004913

5 R-HEM BB1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92//I80846

R-HEM BB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-52:415:81//AF015148

10

R-HEM BB1002218//, complete sequence.//3.4e-17:178:82//AC005300

15 R-HEM BB1002232//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-55:292:88//AC004599

20 R-HEM BB1002247//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//2.9e-13:227:70//AC005829

25 R-HEM BB1002249//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL031733

R-HEM BB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.3e-104:593:91//AC002415

30 R-HEM BB1002255//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930

35 R-HEM BB1002266//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//1.3e-09:371:63//AL010216

40 R-HEM BB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete sequence.//1.3e-39:247:86//AC004534

R-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//4.1e-84:549:86//U73642

45 R-HEM BB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.5e-10:164:71//AC004129

50 R-HEM BB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete sequence.//0.39:365:59//AC005028

55 R-HEM BB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=9 Row=H, genomic survey sequence.//0.96:180:58//B39313

R-HEM BB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete

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sequence.//7.9e-17:258:73//AC004849

- 5 R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//6.9e-96:479:97//AJ010841
- 10 R-HEMBB1002358//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-53:309:83//AC002366
- 15 R-HEMBB1002359//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.9e-27:350:74//AC005038
- R-HEMBB1002364//Homo sapiens Xp22 PAC RPCI1-108M6 (Roswell Park Cancer Center PAC library) complete sequence.//8.6e-53:302:79//AC003036
- 20 R-HEMBB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to chromosome 11, band p13.//3.2e-38:199:100//X04094
- 25 R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:120:78//AF072467
- R-HEMBB1002383//Human DNA sequence from cosmid U19H10 on chromosome X. Contains ESTs and CA repeat.//0.98:351:58//AL021182
- 30 R-HEMBB1002387//HS-1052-B2-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey sequence.//2.0e-07:276:67//B41091
- 35 R-HEMBB1002415//Homo sapiens chromosome 17, clone hRPK.209\_D\_14, complete sequence.//1.4e-25:202:79//AC005730
- 40 R-HEMBB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//3.6e-60:401:87//AC004799
- 45 R-HEMBB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence.//3.1e-51:358:81//AC006046
- R-HEMBB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING DRAFT SEQUENCE.//1.4e-115:557:98//AL034349
- 50 R-HEMBB1002457//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//6.3e-37:338:80//AL031012
- 55 R-HEMBB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//9.7e-09:314:64//AE000659
- R-HEMBB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII

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project).//0.42:110:74//AL021635

- 5 R-HEM BB1002489//Salvelinus fontinalis microsatellite sequence SFO-12.//6.6e-06:167:71//U50302
- 10 R-HEM BB1002492//RPCI11-74F21.TK RPCI11 Homo sapiens genomic clone R-74F21, genomic survey sequence.//3.1e-14:410:63//AQ238960
- 15 R-HEM BB1002495//HS\_3220\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence.//1.3e-24:137:100//AQ180762
- 20 R-HEM BB1002502//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//9.6e-81:538:86//AC006120
- 25 R-HEM BB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.0061:482:57//AL031313
- 30 R-HEM BB1002510//HS\_2179\_A1\_F03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence.//6.9e-35:423:72//AQ298309
- 35 R-HEM BB1002520//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//2.0e-62:201:85//AL033397
- 40 R-HEM BB1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence.//0.99:323:58//AC004225
- 45 R-HEM BB1002531
- 50 R-HEM BB1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.0e-61:380:79//AP000009
- 55 R-HEM BB1002545//RPCI11-2F3.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2F3, genomic survey sequence.//3.5e-12:414:63//B63283
- 60 R-HEM BB1002550
- 65 R-HEM BB1002556//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.6e-62:299:85//AC006160
- 70 R-HEM BB1002579//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORKING DRAFT SEQUENCE.//1.7e-42:286:88//AL034422

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- R-HEM BB1002582//Homo sapiens clone DJ1119N05, complete sequence.//3.0e-14:426:60//AC004968
- 5 R-HEM BB1002590//Homo sapiens clone RG132J19, complete sequence.//1.1e-30:392:74//AC005163
- 10 R-HEM BB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//8.5e-44:335:83//AL021707
- 15 R-HEM BB1002600//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-105:470:96//AC005865
- R-HEM BB1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//1.3e-44:445:77//AC004223
- 20 R-HEM BB1002603//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//7.0e-40:321:82//AC006162
- 25 R-HEM BB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey sequence.//1.1e-44:234:98//AQ060197
- 30 R-HEM BB1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//7.0e-22:455:65//U91321
- R-HEM BB1002613//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.0e-72:302:85//AC005908
- 35 R-HEM BB1002614//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.8e-10:512:60//AC004801
- 40 R-HEM BB1002617//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-24:486:63//AC005520
- 45 R-HEM BB1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.4e-41:326:83//AC004953
- R-HEM BB1002635//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//2.6e-42:360:80//AC005910
- 50 R-HEM BB1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//9.1e-51:335:87//AF042090
- 55 R-HEM BB1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//0.0011:399:59//AF030694

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- 5 R-HEM BB1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//4.1e-55:515:76//AF042090
- R-HEM BB1002684//Human BAC clone RG066D11 from 7q22, complete sequence.//1.7e-18:504:62//AC002430
- 10 R-HEM BB1002686//Homo sapiens full-length insert cDNA clone ZC65D06.//7.0e-85:413:99//AF086217
- R-HEM BB1002692//Homo sapiens 12p13.3 BAC RPC111-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.8e-69:505:82//AC006206
- 15 R-HEM BB1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.26:390:58//AC004153
- 20 R-HEM BB1002699//Human NFE genomic fragment.//8.0e-32:226:79//M98511
- R-HEM BB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey sequence.//8.6e-43:351:8011859764
- 25 R-HEM BB1002705//Plasmodium yoelii rhoptry protein, complete cds.//0.0064:454:59//L27838
- 30 R-HEM BB1002712//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//9.6e-09:187:67//Z98052
- 35 R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.1e-21:201:80//AC005037
- R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence.//4.2e-48:306:82//AF015720
- 40 R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//1.4e-41:306:86//AL022163
- 45 R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.//6.1e-36:281:83//AL031058
- 50 R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.3e-67:321:88//AC000090
- 55 R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.//6.7e-86:559:86//AC004054

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R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicro1.//0.79:63:77//AF025889

5

R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence.//1.6e-53:397:83//AL021366

10

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R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.0e-37:295:83//AC005057

20

R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//7.1e-45:296:88//AC005867

25

R-MAMMA1000085

R-MAMMA1000092//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//8.2e-34:539:69//AL034410

30

R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//3.4e-39:297:85//AC003976

35

R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5.//2.6e-07:162:67//U69641

40

R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.1e-13:141:80//AC004882

R-MAMMA1000133

45

R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.7e-18:171:80//AC005328

50

R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-49:366:75//AC005000

55

R-MAMMA1000143//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC D9.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615

R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-

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- 13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//2.1e-68:562:78//AL022476
- 5
- R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.3e-06:408:58//AC005089
- 10
- R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381
- 15
- R-MAMMA1000173
- R-MAMMA1000175//H.sapiens CpG island DNA genomic Mse1 fragment, clone 186c5, reverse read cpg186c5.rt1b.//0.072:90:72//Z57594
- 20
- R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//1.5e-44:445:75//AC004552
- 25
- R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//1.9e-23:135:85//AF038667
- 30
- R-MAMMA1000221//HS\_3242\_B2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence.//0.031:167:67//AQ220385
- 35
- R-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL031728
- 40
- R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//6.2e-07:445:59//AL022401
- 45
- R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence.//1.6e-25:390:69//AC005266
- 50
- R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//1.1e-37:327:80//AL008715
- 55
- R-MAMMA1000257//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//1.3e-22:281:74//AL034549

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- 5 R-MAMMA1000264//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.7e-29:337:67//AC003656
- 10 R-MAMMA1000266//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//7.7e-37:339:80//AL031670
- 15 R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.2e-40:283:86//AF001549
- 20 R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence.//3.0e-29:265:80//B49900
- 25 R-MAMMA1000278//Sequence 25 from patent US 5708157.//2.6e-39:282:82//I80056
- 30 R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494
- 35 R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone 2522B20, genomic survey sequence.//1.8e-11:288:61//AQ280722
- 40 R-MAMMA1000287
- 45 R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//4.1e-16:169:77//AC005553
- 50 R-MAMMA1000307//RPCI11-89L1.TV RPCI11 Homo sapiens genomic clone R-89L1, genomic survey sequence.//1.3e-86:429:97//AQ284795
- 55 R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00020:384:60//AF029779
- 60 R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequence.//0.0026:310:60//AF003518
- 65 R-MAMMA1000313//Human cosmid Xq28\_IA649, complete sequence.//1.5e-26:317:67//U82694
- 70 R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-39:277:86//AC004947
- 75 R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence.//3.2e-44:180:89//AF015147



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R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.97:293:64//AE001388

- 5 R-MAMMA1000348//Homo sapiens BAC129, complete sequence.//4.4e-27:365:72//J85195
- R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.73:332:61//AC002493
- 10 R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//4.6e-80:279:89//AC005189
- 15 R-MAMMA1000361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING DRAFT SEQUENCE.//7.8e-18:346:63//AL031676
- 20 R-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//5.3e-40:299:83//AL022344
- R-MAMMA1000385//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING DRAFT SEQUENCE.//1.0e-28:225:84//AL031658
- 25 R-MAMMA1000388//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//4.7e-60:298:99//AQ038102
- 30 R-MAMMA1000395
- R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence.//1.4e-84:276:88//AC004692
- 35 R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//6.7e-35:360:76//AC002394
- 40 R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//3.1e-69:327:79//AC004662
- 45 R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chromosome Xq13.1-Xq21.2. Contains GSS (BAC end sequence),STS.//3.6e-41:180:87//AL009028
- R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.1e-59:478:77//AC005377
- 50 R-MAMMA1000421//Human coxVIb gene, last exon and flanking sequence.//5.3e-53:294:82//X58139
- 55 R-MAMMA1000422//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING DRAFT SEQUENCE.//1.0:252:59//AL031737

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- R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence.//2.0e-50:491:76//AC004816
- 5 R-MAMMA1000424//Human DNA sequence from PAC 507115 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//3.5e-40:340:80//Z98950
- 10 R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//0.0019:87:79//AF062484
- R-MAMMA1000431//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.0e-58:564:77//AC004821
- 15 R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//3.0e-43:328:83//AC002067
- 20 R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequence.//0.95:209:65//U82672
- R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence.//0.99:182:61//AB019236
- 25 R-MAMMA1000468
- 30 R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9N34, genomic survey sequence.//1.0e-38:142:88//AG010148
- R-MAMMA1000478//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//1.3e-37:286:83//Z93015
- 35 R-MAMMA1000483//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//4.3e-34:158:86//B54637
- 40 R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//4.2e-98:569:90//AC006130
- 45 R-MAMMA1000500//Human BRCA1, Rho7 and vatI genes, complete cds, and ipf35 gene, partial cds.//1.2e-41:334:79//L78833
- R-MAMMA1000501//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//1.4e-38:250:84//AL031118
- 50 R-MAMMA1000516//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//1.3e-43:318:83//Z82207
- 55 R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.//4.4e-13:202:73//AL031289

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- 5 R-MAMMA1000559//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//2.2e-30:245:83//Z93015
- 10 R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01\_183\_B\_7 map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:80//U82205
- 15 R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds.//9.2e-19:216:76//U18419
- 20 R-MAMMA1000576
- 25 R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//5.4e-53:297:85//AC005666
- 30 R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-35:450:71//AC006018
- 35 R-MAMMA1000594//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from cosmid 5L5, WORKING DRAFT SEQUENCE.//4.3e-26:293:75//AJ009613
- 40 R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey sequence.//0.83:110:70//AQ057131
- 45 R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.6e-50:290:86//AC004956
- 50 R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey sequence.//0.76:132:65//AQ038364
- 55 R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//U06970
- R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573
- R-MAMMA1000623
- R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//AC005498
- R-MAMMA1000643//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39B17, WORKING DRAFT SEQUENCE.//1.4e-06:236:68//AL023656
- R-MAMMA1000664//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0326F06; HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555

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- 5 R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:86//AL021578
- 10 R-MAMMA1000670
- R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//AL031785
- 15 R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63//AF054623
- R-MAMMA1000696//Human Chromosome X clone bW XD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.7e-46:464:71//AC004387
- 20 R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-09:244:66//AC005075
- 25 R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-51:439:74//AC005478
- R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete sequence.//2.8e-29:288:75//AC004694
- 30 R-MAMMA1000718//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics) , PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//3.0e-37:231:91//AC002366
- 35 R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//1.4e-35:299:81//AC005781
- 40 R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//3.9e-59:409:79//AL022163
- 45 R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.4e-29:560:66//AC005077
- 50 R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.4e-14:309:68//AC004832
- 55 R-MAMMA1000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//4.1e-29:377:71//AL008722
- R-MAMMA1000734//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone

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191J18, WORKING DRAFT SEQUENCE.//2.0e-108:420:99//AL024507

- 5 R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus.//6.6e-41:347:82//U03115
- 10 R-MAMMA1000744//T27O8-T7 TAMU Arabidopsis thaliana genomic clone T27O8, genomic survey sequence.//0.095:367:60//B20150
- 15 R-MAMMA1000746//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//7.4e-95:569:87//AC004661
- R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.3e-48:295:84//AC003071
- 20 R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//5.7e-45:347:82//Z82178
- 25 R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.1e-32:292:80//U73169
- 30 R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.5e-50:467:79//AC005412
- R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//1.0e-63:429:79//AC002454
- 35 R-MAMMA1000778//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//3.5e-25:234:81//Z95704
- 40 R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//0.0021:119:74//AL031120
- 45 R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3.//6.3e-08:269:64//AJ229042
- R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//1.1e-36:261:80//AC005339
- 50 R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence.//0.68:156:65//AQ240807
- 55 R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726\_O\_12, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.6e-50:335:86//AC005517
- R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete

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sequence.//1.3e-40:322:77//U91323

5 R-MAMMA1000842//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//4.1e-44:471:74//Z97985

10 R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.85:394:60//AC004815

10 R-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.54:303:63//AL031744

15 R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence.//1.7e-10:115:83//AF030876

20 R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//5.0e-44:352:83//AC004263

25 R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence.//1.8e-10:149:74//AC00461

25 R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16.//8.1e-05:205:66//AF009075

30 R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//2.9e-49:421:80//AC002364

35 R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//9.1e-41:302:83//AC002301

40 R-MAMMA1000867//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds.//1.9e-17:500:61//L78833

40 R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequenced.//1.2e-17:211:74//AC004653

45 R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//4.7e-09:160:65//AC003658

50 R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.2e-34:354:75//Z93023

55 R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.4e-41:411:74//AC002425

R-MAMMA1000883

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R-MAMMA1000897

5 R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence.//1.3e-73:304:91//AC004506

10 R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110

R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ416i6, complete sequence.//1.5e-09:170:71//AC003024

15 R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//8.3e-13:323:67//AC005247

20 R-MAMMA1000921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL034379

25 R-MAMMA1000931//HS\_3227\_B1\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence.//1.4e-55:443:79//AQ191777

30 R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:340:84//AC005046

R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.8e-53:330:84//AC002347

35 R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:391:74//AC004383

40 R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.6e-75:566:81//AC002477

45 R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//0.013:285:59//AL034559

R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.2e-45:288:90//AC005096

50 R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-108:561:96//AC006001

55 R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.9e-41:287:87//AC004263

R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome

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6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152

5

R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//3.2e-34:296:80//AJ011930

10

R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219

15

R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190

20

R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101

25

R-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929

30

R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence.//3.8e-39:286:87//AC004910

35

R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-31:274:80//AC004913

40

R-MAMMA1001030//Homo sapiens full-length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074

45

R-MAMMA1001035//RPCI-1-46G8Sp6 RPCI-1 Homo sapiens genomic clone RPCI-1-46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285

50

R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089

55

R-nnnnnnnnnnnnn

R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394

R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence.//7.2e-65:946:95//AQ111326